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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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         SPTREMBL 21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassifie
15: sp_archeap:*
17: sp_archeap:*
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sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vrurus:*
sp_rvirus:*
sp_rvirus:*
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sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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# ALIGNMENTS

M B Q	RESULT O93413 AD	!
Query Match 41.8%; Score 901; DB 13; Length 363; Best Local Similarity 50.3%; Pred. No. 6.7e-68; Matches 179; Conservative 56; Mismatches 77; Indels 44; Gaps 5;	O3413 PRELIMINARY; PRT; 363 AA. O3413; O93413; O1-NOV-1998 (TREMBLrel. 08, Created) O1-NOV-1998 (TREMBLrel. 08, Last sequence update) O1-NOV-1998 (TREMBLrel. 21, Last annotation update) O1-NOV-1998 (TREMBLREL) C1-NOV-1998 (TREMBLREL) C2-NOV-1998 (TREMBLR	

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Query Match
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Sphoeroides.
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PRINTS; PR01565; NEUROWEDINUR.
PRINTS; PR01566; NEUROMEDNUUR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
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InterPro; IPR000524; HTH_GntR.
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ATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLMAVALLSAGPFLFLVGVEQDP
                                                                                                                                        GRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTY
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                                                                                                                                                                                                                                                                                                                    187;
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                                                                                                                                                                                                                                                                                                                                                                                                                            374 AA;
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                                                                                                                                                                                                                                                                                                                                           39.2%; Score 845;
45.5%; Pred. No.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1;

PROSITE; PS50262; G PROTEIN RECEP F1 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           093414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     093414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Endocrinol. 14:160-169
EMBL; AF082211; AAC33474.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretagogue receptor (GHS-R) conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20092336; PubMed=10628755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Ligand activation domain of human orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                    139
                                              192 -NGTARIASSPLASSPPLWLSRAPPPSPPSGPE----TAEAAALFSRECRPS--PAQLGA 244
                                                                                                        199
                                                                                                                                                                                                                                                                           139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLGALRVMLWVTTAYFFLFFLCLSILYGLIGRELWSSRRPLR-GPAASGRERGHRQTKRV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _TaxID=39110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMSWKYRGAVARLFGVSDSPPQ---RGR-TASTVKMD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĹVVVVĽAFVĽCWĽÞFHVGRYLQFRSLDAPSPLLSLLŚEÝCSLVSVVĽFYĽSAAINPILYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLVVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLSASINPILYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGKEGEKGFIIGERERENRDKGLKDEQLEEMNWKDKEMNECGDKNGVTKGFKGGDKSLEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                           LHKCSNQECHWEEPV-FGMIVCVTIIYIPLMLFGLLGNILTILVVWLRPYMRSSTYLYLS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPPCDERRC---SPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLG
                                                                                                                                                                                                                    AICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE----QDPGIS-----
                                                                                                                                                                                                                                                                                                                                                                                 SWĄVSDLIILIGIPFDLYRIWRSRPWVFGPLLCRLSLYVGEGCTYATLIHMTALSVERYL
                                                                                                                                                                                                                                                                                                                               SLAVSDILILLLEVDLYKLWRPRPWPFGEIFCKSTMFFSECCTFCSILHITFISLERYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4:160-169(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 602; DB 13; 29.5%; Pred. No. 1.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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UNKNOWN\_1

Length 559;

Indels

180;

Gaps

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186 138

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191

growth hormone pufferfish to

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Hreniuk D.L.,

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RESULT 093412

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RESULT 4

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                                                                                                     Query Match
Best Local Sim:
Matches 129;
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                                                                                                                                                                                                                                                             HSSP; P02699; 1F88;
HSSP; P02699; 1F88;
InterPro; IPR00076; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR01237; GFCRRHODOPSN.
PRINTS; PR012565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDINUR.
PRINTS; PR01570; NPFFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 24-426 FROM N.A.

MEDLINE=99000845; PubMed=9782091;
Tan C.P., McKee K.K., Liu Q., Palyha O.C., Feighner S.D.,
Hreniuk D.L., Smith R.G., Howard A.D.;
"Cloning and characterization of a human and murine T-cell
protein-coupled receptor similar to the growth hormone secr
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20490668; PubMed=10899166;
Raddatz R., Wilson A.E., Artymyshyn R., Bonini J.A., Borowsky B.,
Boteju L.W., Zhou S., Kouranova E.V., Nagorny R., Guevarra M.S.,
Dai M., Lerman G.S., Vaysse P.J., Branchek T.A., Gerald C., Forra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9HB89; O43664;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neuromedin U receptor 1 (Orphan G protein-coupled receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF044600; AAC02680.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Differentially Expressed in Peripheral Tissues and the Central Nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9НВ89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and Characterization of Two Neuromedin U
39 VPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILL-GLPFDLYR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 275:32452-32459(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLAR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEAQTGRGDGGRAVLDTRGTEARSDGEAAGPSTPEATTADPYDAENSTPLDDTHSHSQYF 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVFVLCWLPFHVGRTIFFFSLGSDRPGVNASHALLDSRVPLELPPPGALGESDEAAGDAF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVLLVVV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSAMLVLSNMYFLVPLCILGLVYGLIGRTLW-----LRS-QISRRDVNNRNTVKMLGVIV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEGTKEQEHGERAAEGEEAQNKMKEDEGGGGGGGGTDGGGRMQVDTRECRCTDYAVSSGL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAFIICWLPFHVGRIIY------INTE----DSR-------
                                                                                                                                        Similarity
                                                                                                                                                                                                                       426 AA; 47350 MW; F8DD781C020F04AA CRC64;
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                              22.5%; Score 484.5; 33.7%; Pred. No. 9.
                                                                                                     63; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426
                                                                                                                                 9.5e-33;
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                                                                                                                                                       DB 4; Length 426;
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Forray
                                                                                              Gaps
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                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                        PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01567; NEUROMEDINUR.
PRINTS; PR01570; NEPFERCEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of murine neuromedin U R2 receptor."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY057384; AAL26695.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Funes S., Hedrick J.A., Yang S., Gustafson E.L.;
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91Z76;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuromedin U receptor type 2. Mus musculus (Mouse).
149 ESTRRALRILSLVWSFSVVFSLPNTSIHGIKFQQFPNGSSVPG-----SATCTVTK 200
                                   149 LVTRRRVRALIAVLWAVALLSAGPFLFLVGV--EQDPGISVVPGLNGTARIASSPLASSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91Z76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 Y--INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLL----LARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                      CSPFPLGALVEVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLI-L 88
                                                                                                    LGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148
                                                                                                                                      CGPKRSDLSLPVSVVYALIFVVGVIGNLLVCLVIARHQTLKTPTNYYLFSLAVSDLLVLL 88
                                                                     LGMPLEVYELWHNYPFLFGPVGCYFKTALFETVCFASILSVTTVSIERYVAIVHPFRAKL
                                                                                                                                                                                                               115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRPRHSSHSLSRMTTGSTLCDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRPR--GFHRSRDTAGEVAGDTG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSVVSQWTDGLHLAFQHVHVISGIFFYLGSAANPVLYSLMSSRFRETFQEALCLGACCHR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RERLLLMQEAKGRGSAAARSRYTCRLQQHDRGRRQVTKMLFVLVVVFGICWAPFHADRVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSRRPL-----RGPAAS------GRERGHRQTKRVLLVVVLAFIICWLFFHVGRII 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPICATYLLIFVVGAVGNGLTCLVILRHKAMRTPTNYYLFSLAVSDLLVLLVGLPLELYE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MWHNYPFLLGVGGCYFRTLLFEMVCLASVLNVTALSVERYVAVVHPLQARSMVTRAHVRR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCRGPVPDSAVCMLVRP-----RALYNMVVQTTALLFFCLPMAIMSVLYLLIGLRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLGAVWGLAMLCSLPNTSLHGIRQ---LHV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTA--YFFLPFLCLSILYGLIGRELW
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                             395 AA; 44844 MW;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                        22.1%; Score 475.5; 30.6%; Pred. No. 5e-tive 79; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402
                                                                                                                                                                                                                                                                             OBB540024566903D CRC64;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shan L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA
                                                                                                                                                                                                                             5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bayne M., Monsma F.J.
                                                                                                                                                                                                                                          DB 11; Length 395;
                                                                                                                                                                                                           101; Indels
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                                                                                                                                                                                                      81;
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Best Local
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01-DEC-2001 (TrEMBLrel. 20
01-JUN-2002 (TrEMBLrel. 20
Neuromedin U receptor 2.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96AM5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01567; NEUROMEDUZR.
PRINTS; PR01570; NEPFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYGLIGREL------WSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PMWV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSPSCKWCHPQHRPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHVGRIIYINTEDSRMMYFSQYFN---IVALQLFYLSASINPILYNLISKKYRAAAFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYYLMGLRLKRDESLEADKVTVNIHRPSR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LA-----RKSRPRG
                                                                                                                                                                                                                                                                                                                                    LVTRRRVRALIAVLWAVALLSAGPFLFLVGVE--QDPGISVVPGLNGTARIASSPLASSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSPEPLGALVPVTAVCLCLFVVGVSGNVVTVMLjGRYRDMRTTTNLYLGSMAVSDLLI-L
                                                                                                                                                                                                                                                                                                                                                                                                                              LGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL
                                        FHVGRIIYINTED-SRMMYFSQYFNIVAL---QLFYLSASINPILYNLISKKYRAAAFKL
                                                                                                                                            LYGLIGRELWSSR-----
                                                                                                                                                                                               PMWI ----
                                                                                                                                                                                                                                       PLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI
                                                                                                                                                                                                                                                                                         QSTRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPG-----
                                                                                                                                                                                                                                                                                                                                                                                      LGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKL
FHIDRLFFSFVEEWSESL--AAVFNLVHVVSGVFFYLSSAVNFIIYNLLSRRFQ-AAFQN
                                                                                               LYYLMALRLKKDKSLEADEGNANIORPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.0%;
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19, Last sequence up
21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                            ----RPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 475; DB 4;
Pred. No. 5.8e-32;
8; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                               -----YNFIIQVTSFLFYLLPMTVISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30BFEDD706436AB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KSVTKMLFVLVLVFAICWTP
                                                                                                    -KSVNKMLFVLVLVFAICWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                 -SATETVIK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
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RESULT

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Q9GZQ4; Q9NRA6;
01-MAR-2001 (Tri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Neuromedin U receptor 2 (Neuromedin U receptor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor TGR-1).
NMUR2 OR NMU2R OR TGR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
Wang S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shan L., Qiao X., Crona J.H., Behan J., Wang S., Gustafson E.L., Monsma F.J. Jr., Hedrick J.A.; "Identification of a Novel Neuromedin U Receptor the Central Nervous System.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boteju L.W.,
Dai M., Lerm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                             "Identification and Functional Characterization of Neuromedin U Receptor.";
J. Biol. Chem. 275:29528-29532(2000).
EMBL, AP272363; AAG24794.1; -.
EMBL; AF292402; AAG03064.1; -.
EMBL; AF292404; AAF82755.1; -.
EMBL; AB041228; BAB13721.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20351041; PubMed=10894543; Mellin T.N., Strack A., Guan X.-M., Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M., Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B., Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., Mckee K.K., Stair J.N., Wcdonald T.P., Lynch K.R., Evans J.F., Austin C.P., Caskey T., van der Ploeg L.H T., Liu Q., Caskey T., van der Ploeg L.H T., Liu Q., "Identification of receptors for neuromedin U and its role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  System.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and Characterization of Two Neuromedin U Receptors
Differentially Expressed in Peripheral Tissues and the Central Nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raddatz R., Wilson A.E., Artymyshyn R., Bonini J.A., Bonteju L.W., Zhou S., Kouranova E.V., Nagorny R., Guevan Dai M., Lerman G.S., Vaysse P.J., Branchek T.A., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20490668; PubMed=10899166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 4-415 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pang L., W
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11010960;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caskey T., van der Ploeg L.H.
"Identification of receptors
                         PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01567; NEUROMEDINUZR.
PRINTS; PR01570; NPFFRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                  Hosoya M., Moriya T., Kawamata Y., Ol
Shintani Y., Fukusumi S., Habata Y.,
                                                                                                                                                                                                                                                                                                                                                                                 Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10887190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 4-415 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       feeding.";
                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
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                                                                                                                                      PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406:70-74 (2000).
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     PS00237; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275:32452-32459(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laz
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  PROTEIN_RECEP_F1_1; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hedrick J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                       , Ohkubo S., Fuj
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                                                                                                                                                                                                                                                                                                                                                                                                             Fujii R., Matsui H., ., Onda H., Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Subtype
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Gerald C., I
                                                                                                                                                                                                                                                                                                                                                                   a Novel Subtype
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Best Local
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Q9JIB1;
01-OCT-2000
                    PEAM; PF00001; 7tm 1; 1.

PRINTS; PR01237; GFCRRHODDFSN.
PRINTS; PR01565; NEUROMEDIUUR.
PRINTS; PR01570; NEUROMEDIUZR.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                    MEDLINE=20351041; PubMed=10894543;
Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M.,
Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,
Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., Mckee K.K.,
Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austin C.P.,
Caskey T., van der Ploeg L.H.T., Liu Q.;
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-JUN-2002 (TrEMBLrel. 15, Last sequence update)
Neuromedin U receptor 2.
NMUZR.
                                                                                                                     InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                 EMBL; AF242875; AAF82756.1;
                                                                                                                                                                 Nature
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                       "Identification of receptors for neuromedin U and its role in
                                                                                                                                                                                                                                                                                                   STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 VIS----SFHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLARKSRPRGFHR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHIDRLFFSFVEEWSESL--AAVFNLVHVVSGVFFYLSSAVNPIIYNLLSRRFQ-AAFQN 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLWLSRAPPPSSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVTRRRVRALIAVLWAVALLSAGPFLFLVGVE--QDPGISVVPGLNGTARIASSPLASSP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLI-L 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMWI -----
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                                                                                                                                                               406:70-74 (2000)
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395 AA; 44722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 AA;
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                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
01D3765B5D5355C0 CRC64;
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                        Query Match
Best Local :
          Matches
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Best Local Similarity
                                                                        SEQUENCE
                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01567; NEUROMEDINUR.
PRINTS; PR01570; NEPFERCEPTOR.
PRINTS; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9ESQ4, PRELIMINARY, PRT; 395 AA.
O9ESQ4, O1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                              Neuromedin U Receptor.";
J. Biol. Chem. 275:29528-29532(2000).
EMBL; AB041229; BAB13722.1; -.
                                                                                                                                                                                                                                                                                                     Fujino M.;
                                                                                                                                                                                                                                                                                                          HOSOYA M., Moriya T., Kawamata Y., Ohkubo S., Fujii R., Matsui H.,
Shintani Y., Fukusumi S., Habata Y., Hinuma S., Onda H., Nishimura
                                                                                                                                                                                                                                                                                                                              MEDLINE=20449029; PubMed=10887190; Hosoya M., Moriya T., Kawamata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor TGR-1.
                                                                                                                                                                                                                                                                             "Identification and Functional Characterization of a Novel Subtype
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 RPQG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 LYGLIGRELWSSRRPLRGPAASGRERGHRQT-KRVLLVVVLAFIICWLPFHVGRIIYINT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 LVTRRRVRALIAVLWAVALLSAGPFLFLVGV--EQDPGISVVPGLNGTARIASSPLASSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
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      107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ED--SRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLA-----RKS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEWTESLAAVFNLIHVVSGVFFYLSSAVNPIIYNLLSRRFR-AAFRNVVSPTCKWCHPRH 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYYLMGLRLKRDESLEANKVAVNIHRPSRKSVTKMLFVLVLVFAICWTPFHVDRLFFSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMWV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGMPLEIYEMWHNYPFLFGPVGCYFKTALFETVCFASILSVTTVSVERYVAIVHPFRAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGPKRSDLSLPVSVAYALIFLVGVMGNLLVCMVIVRHQTLKTPTNYYLFSLAVSDLLVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLI-L
                      Similarity
                                                                  395 AA; 44756 MW; EABD6D36E9C355DA CRC64;
      Conservative
                 21.8%; Score 470.5; DB 31.2%; Pred. No. 1.3e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.9%; Score 472.5; DB 1
30.5%; Pred. No. 8.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Mismatches 115;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YNLIIQATSFLFYILPMTLISV
                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 395;
                                                                                                                                                                                                                                                                                                            Onda H., Nishimura O.,
   Indels
                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
   49;
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Gaps
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30 CSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLI-L 88

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RESULT 10
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01-JUN-1998 (TrEMBLrel. 06, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                EMBL; AF044602; AAC02681.1; -.

MGD; MGI:1341898; Gpr66.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01566; NEUROMEDINUR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orphan G protein-coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   055040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 055040
                                                                                                                                                                                                                                                                                                                                                                                                                                                   McKee K.K., Tan C.T., Liu J., Palyha O.C., Feighner S.D. Hreniuk D.L., Smith R.G., Howard A.D.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF044602; AAC02681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
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                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                            130
 186
                              190
                                                                                                                     70
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                                                                                                                                                                                 10
                                                                                                                                                                                                          19 WPALPP----CDE----RRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMR 70
                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESTREBALRILSLVWSFSVVFSLPNTSIHGIKFQHFPNGSSVPG-----SATCTVTK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVTRRRVRALIAVLWAVALLSAGPFLFLVGV--EQDPGISVVPGLNGTARIASSPLASSP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYGLIGRELWSSRRPLRGPAASGRERGHRQT-KRVLLVVVLAFIICWLPFHYGRIIYINI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEWTESLAAVFNLIHVVSGVFFYLSSAVNPIIYNLLSRRFRAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYYLMGLRİKRDESLEANKVAVNIHRPSRKSVTKMİFVLVİVFAİCWTPFHVDRLFFSFV 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ED--SRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAA 365
                                                                                                                   TPTNFYLFSLAVSDMLVLLVGLPLELYEMQQNYPFQLGASACYFRILLLETVCLASVLNV 129
                                                                                                                                      TTINLYLGSMAVSDLLILL-GLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHM 129
                                                                                                                                                                               WPYQPEDLNLTDEALRLKYLGPQQMKQFVPICVTYLLIFVVGTLGNGLTCTVILRNKTMR
                                                         TALSVERYVAVVRPLOAKSVMTRAHVRRMVGAIWVLATLFSLPNTSLHGLSO----LTVP
                            GLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVML
                                                                                     TALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVP 189
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                      405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                        45609 MW; F1BA493D3EB81F34 CRC64;
                                                                                                                                                                                                                                                           21.2%;
                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                           Score 456.5;
Pred. No. 2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
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                                                                                                                                                                                                                                                                             DB 11;
    -SAICS---LVGPMDFYKL-VVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                141; Indels
                                                                                                                                                                                                                                                                             Length
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         210
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Best Local S
Matches 109
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
                                                                                                                                                                                                                                                                                                          "Direct Submission."; Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF025463; AAB71009.1; -
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sammons L., Wohldmann P., Antoniou B.; "The sequence of C. elegans cosmid K10B4."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 47.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329
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                                                                                                                                                                                                                                                                                                                                                                            Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 418 AA; 4
                                                                                                                                                                                                                                                     PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01565; NEUROMEDININ RECEP_F1_1;
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
142 KIFSTLWRANVLIILAWTISFVCALPIAFIVQINKLPLPEDAKYQPWTNKVSFFAVGVLN
                          147 RVLVTRRRVRALIAVLWAVALLSAGÞFLFLVGVEQDÞ---GISVVÞGLNGTARIASSÞLA 203
                                                                                                               24
                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANPVLYSLMSTRFRETFLOALGLGTQCCHRRQPYHGSHNHIRLTTGSTLCDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTALLFFCLPMVTISVLYLLIGLRLRRERMLLQVEVKGRKTAATQETSHRRIQLQDRGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WVTTAYFFLPFLCLSILYGLIGRELWSSRRPL-----RGPAASG------RERGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPILYNLISKKYRAAAFKLL-----LARKSRPRGFHRS-RDTAGEVAGDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVTXMLFALVVVFGICWAPFHADRIMWSLVYGHSTEGLHLAY--QCVHIASGIFFYLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTKRVLLVVVLAFIICWLPFHVGRIIYI-----NTEDSRMMYFSQYFNIVALQLFYLSAS
                                                                                 LLGLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTYATLLHWTALSVERYLAICRPLRA 146
                                                                                                             RCQ--SAGIVIPTVIIYGTIFLLGLFGNICTCIVIAANKSMHNPTNYYLFSLAVSDIIAL 81
                                                                                                                                      RCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLVLGSMAVSDLL-I 87
                                                       ILGLPMETYQSLDYSYPYRFSEGICKARAFLIEFTSYASIMIICCFSFERWLAICHPLRS 141
                                                                                                                                                                   109;
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kDa protein.
                                                                                                                                                                                                                            47735 MW; CE0416539CA3BB27 CRC64;
                                                                                                                                                                                   20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The C. elegans
                                                                                                                                                                        77;
                                                                                                                                                                                      Pred.
                                                                                                                                                                                      Score 434; DB 5;
Pred. No. 1.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing
                                                                                                                                                                                                                                                                     UNKNOWN
                                                                                                                                                                                                   Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consortium
                                                                                                                                                                           Indels
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                                                                                                                                                                            38;
                                                                                                                                                                             Gaps
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RA Adams M.D. (Calniker S.E., Holth R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Hichards S.A., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N., RA Barandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix., RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix., RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix., RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix., RA Burton G.G., Wolson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Gerry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., RA Ge Pablos B., Dalcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Park G.C., Perriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., A Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Mathai B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Land Y., Levitsky A.A., Li J., Li Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Mays A.D., Devi Y., Reese M.G., Pan S., Pollard J., Paleson D.L., Raft C., Mozris J., Moshrefi A., Ra Merkhlov G., Milshinan N.V., Mobarry C., Mozris J., Moshrefi A., Ra Merkhlov G., Milshinan N.V., Mobarry C., Mozris J., Moshrefi A., Ra Anne B.E., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Ra Ra Kimel B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Ra Khue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Ra Kimel S.M., Weissenbach J., Ra Yellon K.H., Shang X., Zhan M., Zhang S., Zhao Q., Zheng L., Shan M., Zhang S., Zhao Q., Zheng L., Shan H.O., Zhang S., Zhao Q., Zheng L., Shan H.O., Zhu S., Zhu S., Zhu S., Zhu X., Smith H.O., Zheng S., Zhu S., Zhu 
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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CG9918
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Ephydroidea; Drosophilidae; Drosophila
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01-JUN-2002
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RESULT 13
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Q9VFW6;
01-MAY-2000
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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Pfam; PF00001; 7tm 1; 1.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
                                                                                                                           STRAIN=BERKELEY;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda;
Pterygota; Neoptera; Endopterygo
                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
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01-JUN-2002
                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                               CG8795
                                                                                                                                                                                                                                                                                           CG8795 protein.
                                                                                                                                                                                 NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 SKGSLNSRN 376
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InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSGAGTAGLMGGSGAQLSSVRGRLNHYGTRRVLRMLVAVVVCFFLCWAPFHAQRLIAIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                 Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GHRQTKRVLLVVVLAFIICWLPFHVGRIIYI- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QCGIVRVIVKHSFQLSTFIFF
                                                                                                                                                                                                                                                                                                                                                                                        595
                                                                                                                                                                                                             Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Bablew R.M., Baswandale J., Bayraktaroglu L., Beasley E.M., RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Bayostein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Land J.A., Ketchum K.A., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. L., RA Kimmel B.E., Stituna N.V., Mobarry C., Morris J., Moshrefi A., RA McHallon D.R., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M., RA Ra Hazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G., RA Ra Hazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G., RA Ra Hazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G., RA Ra Hazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G., RA Ra Hazzolo M., Pittman G.S., Stapleon M., Skupski M.P., Smith T., RA Ra Ra Hazzolo M., Pittman G.S., Stapleon M., Skupski M.P., Smith T., RA Ra Ra Hazzolo M., Pittman G.S., Stapleon M., Skupski M.P., Smith T., RA Ra Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Ra Hazzolo M., Pittman G.S., Zhan M., Zhang G., Zhao Q., Zheng L., Yeh R., P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Parkeri J., McMara G., Zhan M., Zhang G., Zhao Q., Zheng L., La Harden G., Zhan M., Zhang G., Zhao Q., Zheng T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

Transmembrane.
320 -IYINTEDSRMMYFSQYFNIVALQ---LFYLSASINPILYNLISKKYRAAAFKLLLAR--
                                                                                                                                                                                                                                                                                                                                                                                            93 FDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 PLGALVEVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILL-GLP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                GVKLKRSRLLQALPRRCYDVNRGISAQTR-----VIRMLVAVAVAFFICWAPFHAQRIM 300
                                                                                                                                                                                                                                                                                                                                              QDLYNLWHPDNYPFSDSICILESVLSETAANATVLTITAFTYERYIAICHPFRQHTMSKL
                                                                                               GRELWSSR--RPL-----RGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRI-
                                                                                                                                                                                                                                                                                             RRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                             PLSTLATLSVGYALIFIAGVLGNLITCIVISRNNFMHTATNFYLFNLAISDMILLCSGMP 117
                                                                                                                                                                                                APPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFL--PFLCLSILYGLI
                                                                                                                                                                                                                                                 SRAVKFIFAIWIAALLLALPQAIQFSV-----VMQGMGTSCTMKNDFFAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.2%; Score 414; DB 5; 29.7%; Pred. No. 1.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3E8E183BADF5471E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                          ----VFAVSGFLFFGGPMTAICVLYVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                 246
                                                                                                                                                                                                                                                                222
                 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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Q9JIB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JIB2;
Q9JIB2;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X., Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B., Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B., Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., McKee K.K., Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austin C.P., Caskey T., van der Ploeg L.H.T., Liu Q., Liu Q., "Identification of receptors for neuromedin U and its role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuromedin U receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00237; GFCRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDINUR.
PRINTS; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20351041; PubMed=10894543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF242873; AAF82754.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 ----KSRPRGFHRS-----RDTAGEVAGDTGGDTVGYTETSANVKTMG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feeding.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                      151
                       371 LARKSRPRGFHRSR 384
                                                                       291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 PFPLGALVPVTAVCLCLEVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILL-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
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                                                                                                                                                                                                                                                                                                                 -SRAPPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGL
                                                                                                                                                                                                                                                                                                                                                                                                                TRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPLELYEMOHNYPFOLGAGGCYFRILLLETVCLASVLNVTALSVERYVAVVHPLOAKSVM 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHWTALSVERYLAICRPLRARVLV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POQVKQFLPICVTYLLIFVVGTLGNGLTCTVILRQKAMHTPTNFYLFSLAVSDLLVLLVG
                                                                     HADRLMWSMVSHWTDGLRLAF--QSVHLASGVFLYLGSAANPVLYNLMSTRFR-ESFRET
                                                                                                                 HVGRIIYIN----TEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLL 370
                                                                                                                                                                                                                                                                                                                                                                     TRTHVRRMLGAIWVFAILFSLPNTSLHGLS-----
                                                                                                                                                                    IGLRLRRERILLQEEVKGRISAAARQASHRSIQLRDRERRQVTKMLIALVIVFGTCWVPF
                                                                                                                                                                                                                     IGRELWSSR----RPLRGPAASG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406:70-74 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 AA; 45782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.0%; Score 410; DB 11; Length 402; 29.9%; Pred. No. 1.7e-26;
                                                                                                                                                                                                                                                                        --SVTCTLVRPQFFYKLVIQTTILLFFCLPMVTISVLYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB576083D9F7A095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402
                                                                                                                                                                                                                               -RERGHROTKRVLLVVVLAFIICWLPF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                               -----PLYV 184
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B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359
                                                                                                                                                                                                                                                                                                                                      269
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                                                                                                                                                                                         290
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-!- SIMILARITY: BELONGS TO FAMILY 1
EMBL; AE003699; AAF54929.1; --

ဝှု

InterPro; IPR000923; BlueCu 1. InterPro; IPR000276; GPCR\_Rhodpsn. FlyBase; FBgn0038139; CG8795.

PF00001; 7tm\_1;

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> 213 178

Matches

121;

Conservative

61;

Similarity

595 AA;

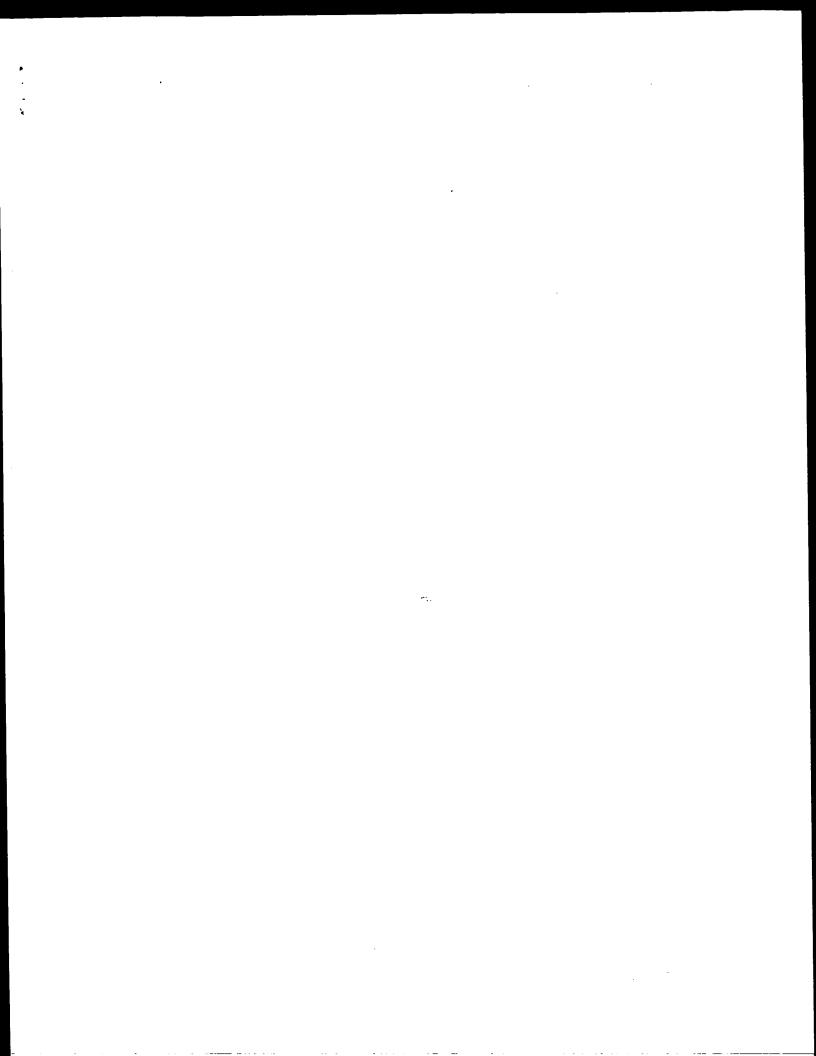
65091 MW;

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Q8TBH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.8%; Score 405; DB 4; Length 410; Best Local Similarity 30.9%; Pred. No. 4.5e-26; Matches 128; Conservative 61; Mismatches 135; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022501; AAH22501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBTBH6;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neurotensin receptor 2.
Homo sapiens (Human)
                                                          331 PLYNFYHYFYMVTNTLFYVSSAVTPLLYNAVSSSFR----RLFLEAVSSLCGEH 380
                                                                                                                                                          272 RELWSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDSR--- 328
                                                                                                                                                                                            239 QVPSTSTP-GSSTPSRLELLSEE-----GLLSFIVWKKT-----FIQG--G 276
                                                                                                                                                                                                                            212 RAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              181 ETADGÉPEPASRYCTVL--VSRTALQVFIQVNVLVSFVLPLALTAFLNGVTVSHLLALCS 238
                                                                                                                                                                                                                                                                                               180 -----EQDPGISVVPGLNGTARIASS------PLASSPPL-------WLS 211
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TBH6
                                                                                                                                                                                                                                                                                                                                                 124 ATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGV---- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FISSUE=BRAIN;
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                                                                              -MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFH 381
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OVSLVRHKDVR-----RIRSLQRSVQVLRAIVVMYVICWLPYHARRLMYCYVPDDAWTD 330
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
      Database :
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Perfect score:
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2156
SwissProt_40:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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pyright. It is produced through a colla e of Bioinformatics and the EMBL outs Institute. There are no restrictions utions as long as its content is in	RITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	Produced by alternative splicing!- TISSUE SPECIFICITY: EXPRESSED ONLY IN THYROID, STOWACH, AND BONE MARROW.	PRODUCT	FUNCTION: Receptor for motilin.	gogue receptor i	eonard R. Bailey A.R.T., Palyha O.C., Feighne	CTION. LINE=21219832: PubMed	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. $\lceil 4 \rceil$	M (	EDOM NI A (TOODS)	Science 284-2184-2188(1900)	т.	Don troop Hilling Brails O., Falcilett A.A.,	Bakshi R., Abramovitz M., Stocco R., Kargman S.,	Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.	99316084; PubMed=10381885;	FROM N.A.	GELUMICS 46:426-434(1997).	otensin receptors.";	ted to the gro	characterization of two human G protein-counled recent	an C.P., Palyha O.C., Liu J.,	MEDLINE=98110578; PubMed=9441746;	VOR FROM N & (TROPON	; Catarrhini; Hominidae; Homo.	ata; Vertebrata	Homo sapiens (Human).	recepto	15-UN-2002 (Rel. 41, Last annotation update)	1998 (Rel. 37, Created)		LT 1 _HUMAN _MTLR HIMAN STANDARD.

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                                                      LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK
                                                                                   QLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTVRVL
                                                                                                       QLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVL
                                                                                                                           QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPA
                                                                                                                                          CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE
                                                                                                                                                                                                             MLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG
                 KYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG
   KYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1.
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99.8%;
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BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

LVVVLAFIICHLPFHVGRIIYINTEDSRMMYFSQYFNIVAL

LVVVLAFIICHLPFHVGRIIYINTEDSRMMYFSQYFNIVAL

QLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHR

SRDTAGEVAGDTGGDTVGYTETSANVKTMG -> RKWSRRG
SKDACLQSAPFGTAQTLGFLFLLAQLMAFLFAFFFISIFAS
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                         Score 2149; DB 1
Pred. No. 3e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
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6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                            TRRGGGSGIYNLLVALPRWQNHLHKHGRFADDVLLSVL
                                                                                                                                                                                                                                                                                                                                         C13FF6165012DEF3 CRC64;
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RESULT 2
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SEGRAIN-Yorkshire; TISSUB=Pituitary;

STRAIN-Yorkshire; TISSUB=Pituitary;

MEDLINE=96337998; PubMed=8688086;

MEDLINE=96337998; PubMed=8688086;

Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,

Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,

Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,

Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

Palyha O.C., Anderson J., Paress P.S., Diaz C., Dean D.C., Melillo D.

McKee K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dean D.C., Melillo D.

Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.

Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;

Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;

"A receptor in pituitary and hypothalamus that functions in growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95254; Q95255; Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Growth hormone secretagogue receptor type 1 peptide receptor) (GHRP) (Ghrelin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone release.";
Science 273:974-977(1996).
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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U60180; AAC48631.1;
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CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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Gupta S.K.,
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth hormone secretagogue receptor type 1 (GHS-R)
peptide receptor) (GHRP) (Ghrelin receptor).
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01-NOV-1997 (Rel) 1= 01-NOV-1997
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Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,
Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,
McKee K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dashkevicz M.,
Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D
Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K
Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pituitary;
MEDLINE=96337998; PubMed=8688086;
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MISSING (IN ISOFORM 1B) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein compled receptor; Transmembrane;
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EMBL; U60181; AAC50654.1; --
EMBL; AF369786; AAK71539.1; --
EMBL; AF369786; AAK71540.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone secretagogue receptor."; Endocrinology 142:2649-2659(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eweropean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content if and this statement is not removed. Usage by and its content in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: PITUITARY AND HYPOTHALAMUS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as well as non-peptide, low molecular weight secre L-692,429, MK-0677, adenosine, SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A (SHOWN HERE) PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 1B APPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 protein Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (GHRP) (e.g. Met-enkephalin and Ghrenout releasing peptides (e.g. Met-enkephalin and Ghrenout releasing peptides (e.g. Met-enkephalin and Ghrenout releasing
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H., Date Y., Nakazato M.,
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   MW.
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15-JUL-1998 (Rel. 36, Creaco.,
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth hormone secretagogue receptor type 1 (
Growth hormone secretagogue receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                      GHSR_RAT
008725;
                                                                                                                                                                                                        Mol
                                                                                                                                                                                                                 MCKEE K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P., Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.; "Molecular analysis of rat pituitary and hypothalamic growth hosecretagogue receptors.";
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                MEDLINE=97246555; PubMed=9092793;
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia;
          Nature 402:656-660(1999)
                                                                                                                                                                      STRAIN=Wistar;
                                                                                                                                                                                SEQUENCE OF 1-240 FROM N.A.
                                                                                                                                                                                                                                                                             TISSUE=Pituitary;
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                        stomach."
                                  "Ghrelin
                                             Kojima M.,
                                                          MEDLINE=20067959;
                                                                                              peptide receptor in rat
Peptides 19:15-20(1998)
                                                                                                           "Molecular cloning and gene expression
peptide receptor in rat tissues.";
                                                                                                                                 Takahara J.;
                                                                                                                                             Yokote R.
                                                                                                                                                        MEDLINE=98100386; PubMed=9437732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
FUNCTION: Receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTVKMLAVVVFAFILCWLPFHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLSAAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTKRVLLVVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLSASIN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGVEHE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTEFAVRSGLLTVMVWVSSIFFFLPVFCLTVLYSLIGRKLWRRRRGDAVVGASLRDQNHK
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                                                                                                                                                                                                           Endocrinol.
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                                  is a growth-hormone-releasing
                                                                                                                                             Sato M.,
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                                                Hosoda
                                                                                                                                                                    TISSUE=Pituitary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                           11:415-423(1997).
                                               н.
                                                PubMed=10604470;
H., Date Y., Nakazato M.,
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 ghrelin,
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Pred. No. 1.9e-48;
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                                                                                                                                               Ohye H., Niimi M., Murao
coupled
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                                     o M., Matsuo H., I
acylated peptide
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                                                                                                                                                                                                                                                                                                                                   Murinae; Rattus
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and G as well as non-peptide, low molecular weight secretagogues (L-692,429, MK-0677, adenosine) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 WNAT--PSEEPEPNVTLDLDWDASPGNDSLPDELLPLFPAPLLAGVTATCVALFVVGISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNGSDGPEGAREP-----PWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSG
                                                                                 RGHROTKRVLLVVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLS
                                                                                                                                                                                                                                                   LVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSSPPSGPETAEAAALFSREC
                                                                                                                                                                                                                                                                                            FVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVIWAVAFCSAGPIFV
                                                                                                                                                                                                                                                                                                                                                                             NLLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPWNFGDLLCKLFQ 119
                                         QNHKQTVKMLAVVVFAFILCWLPFHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLS
                                                                                                                          RATEFAVRSGLITVMVWVSSVFFFLPVFCLTVLYSLIGRKLW--RR--RGDAAVGASLRD
                                                                                                                                                           RPS--PAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG---RE
  ASINPILYNLISKKYRAAAFKLL
                                                                                                                                                                                                           LVGVEHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00237; G PROTEIN RECEP_F1_2; 1.
PS50262; G PROTEIN RECEP_F1_2; 1.
PS50262; G PROTEIN TABLE Glycoproteir
PS50262; G PROTEIN TABLE GOTENTIAL)

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MRL outstation -
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PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                           G-protein coupled receptor;
DOMAIN 1 35
                                                                                                                                                                                                                                                                                                                                                      EMBL; AY056474; AAL13336.1; -. EMBL; AF332997; AAG61141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O99P50; O91Z82;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth hormone secretagogue receptor type 1 (
                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-183 FROM N.A. STRAIN=C57BL/6J; TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                        DOMAIN
                                                                                                                                      TRANSMEM
                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                              PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                            InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129S3/SvImJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by rapid amplification of cDNA ends (RACE)."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHSR
                                                                                                                                                     DOMAIN
                                                                                                                                                                RANSMEM
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 73-257 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kacsoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ហ
                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677, adenosine) (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ritted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
Stimulates growth hormone secretion. Binds also other growth
hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor) (GHRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frohman L.A.,
                                                                                                                                                                          36
59
78
101
126
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                             100
125
148
160
28.5%;
45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kineman R.D.;
                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Ghrelin receptor) (Fragment).
                                                                               CYTOPLASMIC (P
BY SIMILARITY.
N-LINKED (GLCN
N-LINKED (GLCN
                                                                                                                                 4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
 Score 614;
Pred. No.
                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                   CYTOPLASMIC
2 (POTENTIA)
                                                                  N-LINKED
                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                       D6FA21EAB0E30791 CRC64;
                                                               (GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                         moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
 5.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                               ng as its content is in no
            DB 1;
                                                                                                                                                                          (POTENTIAL).
                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                       Glycoprotein. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GHS-R) (GH-releasing
            Length 257;
                                                                                             (POTENTIAL)
                                                                              (POTENTIAL)
                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991
01-FEB-1991
15-JUL-1998
               TRANSMEM
DOMAIN
                                                                       PRINTS; PR00237; GFCRRHODDSN.

PRINTS; PR01479; NEUROTENSINR.

PRINTS; PR01480; NEUROTENSINR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;

Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTR1 RAT
P20789;
                                                                                                                                                                                                           CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral me-
-!- SIMILARITY: BELONGS TO FAMILY 1 C
HIGHEST TO TACHYXININS RECEPTORS.
PIR, JH0164; JH0164.
                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                     MEDLINE=90297956; PubMed=1694443; Tanaka K., Masu M., Nakanishi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotensin
insensitive
                                         DOMAIN
                                                    TRANSMEM
                                                               DOMAIN
                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                    Neuron 4:847-854(1990).
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
   CRANSMEM
                                                                                                                                                                            InterPro;
                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                 receptor.
                                                                                                                                                                                                                                                                                                                            "Structure and functional
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 YVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IJ
                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR THE ASSOCIATED WITH G PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNHK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPS--PAQLGALRVMLMVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGHR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLÞFDLYRLWRSRÞWVFGÞLLCRLSL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATEFAVRSGLLTVMVWVSSVFFFLPVFCLTVLYSLIGRKLW--RR--RGDAAVGSSLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPWNFGDLLCKLFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNAT -- PSEEPEPNVTLDLDWDASPGNDSLSDELLPLFPAPLLAGVTATCVALFVVGISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNGSDGPEGAREP-----PWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSG 55
                                                                                                                                                                 PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137; Conservative
                                                                                                                                                            IPR003985; NT1 rec.
IPR003984; NT rec.
0001; 7tm 1; 1.
                                                                                                                                                                                                IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 36, Last annotation update)
(Rel. 36, Last annotation update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  87
96
121
143
165
                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor) (NTRH)
                                                                                                                                                                                                                                                                                                                           expression
1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                          TRIDECAPEPTIDE NEUROTENSIN.
THAT ACTIVATE A PHOSPHATID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                      membrane protein
1 OF G-PROTEIN CO
                                                                                                                                                                                                                                                                                                                           of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424
                                                                                                                                                                                                                                                                                                                           cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66,
                                                                                                                                                                                                                                                                          PHOSPHATIDYLINOSITOL.
                                                                                                                                                                                                                                     COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DPRD-----TNEC
                                                                                                                                                                                                                                                                                                                           rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                           neurotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
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TRANSMEM DOMAIN

166 189 211 236 261 309 331 373 373 373

CYTOPLASMIC 6 (POTENTIA

(POTENTIAL).

(POTENTIAL)

EXTRACELLULAR (POTENTIAL) 7 (POTENTIAL).

424

7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
PALMITATE (POTENTIAL).

DOMAIN

DOMAIN TRANSMEM DOMAIN TRANSMEM

4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL) CYTOPLASMIC (POTENTIAL).

Query Match Best Local Matches 125;

Similarity

Conservative

58;

Mismatches

Score 498; Pred. No. 2

DB 1; .5e-25;

DISULFID LIPID

88 AA;

47054 MW; 23.1%;

A9C2F7EAF8D9BCD3

CRC64;

CARBOHYD CARBOHYD CARBOHYD DOMAIN TRANSMEM

SEQUENCE

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Snider J., Sano H., Ohta M.;

"Neurotensin receptor type 1.";

"Neurotensin receptor type 1.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS

-ssociated with G profesins THAT ACTIVATE A PHOSPHATIDYLINOSITOI

CALCIUM SECOND MESSENGER SYSTEM.

-i- SUBCELJULAR LOCATION: Integral membrane protein.

-i- SUBCELJULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 VPVTAVCLCLFVVGVSGNVVTVMLIGR---YRDMRTTTNLYLGSMAVSDLLI-LLGLPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYR-LWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                    CWLPYHVRRLMFCYISDEQWTTFLFDFYHYFYMLTNALFYVSSAINPILYNLVSANFRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFL-PFLCLSILYGLIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYNFIWVHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHPFKAKTLMSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLVTAIYLALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLILLLAMPVE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CWLPFHVGRIIYINTEDSR----MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLTVM---VHQAAEQGRVCTVGTHNGLEHSTFNMTTEPGRVQALRHGVLVLRAVVIAFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELWSSRRPLRGPAASGR--------ERGHRQTKR----VLLVVVLAFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTKKFISAIWLASALLAIPMLFTMGLQNRSGDGTHPG-----GLVCTPIVDT-----
                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ATVKVVIQVNTFMSFLFPMLVISILNTVIAN
                                              A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                               Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272
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Best Local
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InterPro; IPR003985, NT1 rec.
InterPro; IPR003984, NT rec.
InterPro; IPR003984, NT rec.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01479; NBUROTENSINR.
PRINTS; PR01490; NEUROTENSINR.
PROSITE; P801480; NEUROTENNIR.
PROSITE; P800327; G PROTEIN RECEP_F1_2; 1.
PROSITE; PS050262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
DISULFID
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB017027; BAA33013.1; -. MGD; MGI:97386; Ntsr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
          322
                                    312
                                                                  262
                                                                                             273
                                                                                                                                                    214
                                                                                                                                                                                 184
                                                                                                                                                                                                            154
                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                          39 VPVTAVCLCLEVVGVSGNVVTVMLIGR----YRDMRTTINLYLGSMAVSDLLI-LLGLPFD
                                                                                                                                                                                                                                                                                               VLVTAVYLALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLILLLAMÞVE
                                                                                                                                                                                                                                        LYNFIWVHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHPFKÄKTLMSRS
                         LPFHVGRIIYINTEDSR----MYVFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAF
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         LPYHVRRLMFCYISDEQWTTFLFDFYHYFYMLTNALFYVSSAİNPİLYNLVSANFRQVFL
                                                               KLTVMVHQAAEQGRGVCTVGTHNSLEHSTFNMSIEPGRVQALRHGVLVLRAVVIAFVVCW
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N-LINKED (GLCNAC...)
BY SIMILARITY.
PALMITATE (POTENTY.
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RESULT NTR1\_M

NTR1 MOUSE

MOUSE

STANDARD;

424

O88319; 16-OCT-2001 16-OCT-2001 16-OCT-2001

(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)

receptor type 1 (NT-R-1).

NCBI\_TaxID=10090;

TISSUE=Brain; SEQUENCE FROM N.A. Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Mus musculus (Mouse) NTSR1 OR NTSR Neurotensin 밁 Ş

380 366

FLSTLACLCPGWRHRRKKRP AFKLLLA-----RKSRP

377

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> 273 232

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                       (See http://www.isb-sib.ch/announce/
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382 STLACLCPGWRRRRKKRP

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KLLLA-----RKSRP

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RESULT NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NEEDLE NE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
-i- FUNCTION: RECEDUADE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL T
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Vita N., Laurent P., Lefort S., Chalon
Gully D., le Fur G., Ferrara P., Caput
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
HIGHEST TO TACHYKININS RECEPTORS.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EMBL; AL357033; CAC14923.1; -.
EMBL; AL035669; CAC12747.1; -.
PIR; S29506; S29506.
HSSP; P02699; 1F88.
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InterPro; IPR003985; NT1 rec.
InterPro; IPR003984; NT_rec.
Pfam, PF00001; 7tm_1; 2.
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382 LCPVWRRRRKRP-AFSRKADS
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                    AFKLLLARKSRPRGFHRSRDT
                                           RRLMFCYISDEQWTPFLYDFYHYFYMVTNALFYVSSTINPILYNLVSANFRHIFLATLAC
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                                                                                                             GRERGHROTKRVLLVVVLAFIICWLPFHV
                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                        118;
                                                                                                                                                                                                                                                                                                                                            Length 418;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT
NTR2_HU
                                                                                   STREET RESTREET             Query Match
Best Local
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095665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vita N., Oury-Donat F., Chalon P., Guillemot M., Kaghad M. Thurneyssen S., Garcia S., Poinot-Chazel C., Casellas P., Le Fur G., Maffrand J.P., Shoubrie P., Caput D., Ferrara R., "Neurotensin is an antagonist of the human neurotensin NT expressed in Chinese hamster ovary cells.";

Eur. J. Pharmacol. 360:265-272(1998).

i. FUNCTION: RECEPTOR FOR THE TRIDECAPERTIDE NEUROTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y10148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99066919; PubMed=9851594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotensin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GFCRRHODOPSN
PRINTS; PR01479; NEUROTENSINR
PRINTS; PR01481; NEUROTENSNZR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Lipoprotein;
G-protein coupled receptor; Transmembrane; Lipoprotein;
DOMAIN 1 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003986; NT2_rec.
InterPro; IPR003984; NT_rec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-JUN-2002
                                                                                      SEQUENCE
                                                                                                                                   DISULFID
                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                        CRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSOCIATED WITH G PROTEINS THAT ACTIVATE CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00001; 7tm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:8040; NTSR2
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 40,
(Rel. 40,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
receptor type 2 (NT-R-2) (Levocabastine-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor)
                                                                                        410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAA71233.1; -.
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                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                 32
64
87
109
131
134
176
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                                                                                        45413 MW;
                 18.9%;
31.2%;
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                                                                                                                                                                                   S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                 Score 407;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC 2 (POTENTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC
                                                                                                                                                               CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                           8C3ADA22BE15FD66
                                                                                                                                      SIMILARITY
3 407; LL
NO. 1.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guillemot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410
                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEUROTENSIN. IT IS
A PHOSPHATIDYLINOSITOL-
                                           Length 410;
                                                                                             CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaghad M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NT2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palmitate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bachy A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Matches
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P70310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurotensin receptor type 2 (NT-R-2) (Low-affinity levocabastine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                      J. Neurosci. 16:5613-5620(1996)
-!- FUNCTION: RECEPTOR FOR THE
                                                                                                                                                                                                                                                                                                        Mazella J., Botto J.-M., Guillemare
Vincent J.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                              MEDLINE=96388216;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sensitive neurotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                  levocabastine-sensitive neurotensin/neuromedin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                         SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED MAXIMALLY IN THE CEREBELLUM,
HYPPOCAMPUS, PIRIFORM CORTEX AND NEOCOTIEX OF ADULT BRAIN.
DEVELOPMENTAL STAGE: EXPRESSED POORLY IN 7-DAY-OLD BRAIN.
EXPRESSION INCREASES AT DAY 15 TO REACH A MAXIMAL LEVEL IN 35-DAY-
SIMILARITY:
HIGHEST TO 7
                                                                                                                                                                               FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATLLHMTALSVERYLAICRELRARVLVTRRRVRALIAVLWAVALLSAGPELELVGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRH-----HVLSLALAGLILLLLVGVPVELYSFVWFHYPWVFGDLGCRGYYFVHELCAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETADGEPEPASRVCTVL--VSRTALQVFIQVNVLVSFVLPLALTAFLNGVTVSHLLALCS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRDMRTTTNLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPRPSSNPGLSLDARLGVDTRLWAKVLFTALYALIWALGAAGNALSVHVVLKARAGRAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPWPALPP---CDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLYNFYHYFYMVTNTLFYVSSAVTPLLYNAVSSSFR----KLFLEAVSSLCGEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVPSTSTP-GSSTPSRLELLSEE-----GLLSFIVWKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129;
                                            BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                       functional
                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
: BELONGS TO TACHYKININS
                                                                                                                                                                                                                                                                                                                                                PubMed=8795617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RIRSLQRSVQVLRAIVVMYVICWLPYHARRLMYCYVPDDAWTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor) (NTRL).
                                                                                                                                                                                                                                                                                       expression, and cerebral localization of the
  FAMILY 1 OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                               ;
H
                       ဝှု
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                         G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                               Coppola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135;
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T.
                                                                                                                                                                                                                                                                    receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----WLS
                                                                                                                                                                                                                                                                          from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 126;
         PAT

NTR2 RAT

Q63384;
Q63384;
01-NOV-1997
01-NOV-1997
16-OCT-2001
  Neurotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003986; NT2_rec.
InterPro; IPR003984; NT_rec.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                              276
                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01481; NEUROTENSN2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:108018; Ntsr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         216
                                                                                                                                                                                                                               246
                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                  127
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                                                                                                                                                                                                                                                                                                                                                                                                              19 WPALP-----PCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRT- 71
                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                              RGPAASGRERGHRQTK-----RVLLVVVLAFIICWLPFHVGRIIYINTED----SRMMY 331
                                                                                                            FYHYFYMVTNTLFYVSSAVTPVLYNAVSSSFR----KLFLESLSSLCGEQRS
                                                                                                                                     FSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRS
                                                                                                                                                           GVQASLVRHKDASQIRSLQHSAQVLRAIVAVYVICWLPYHARRLMYCYIPDDGWTDELYD
                                                                                                                                                                                                                           RVMLWVTTA-----YFFLPFLC-----LSIL--YGLIGRELWSSRRPL
                                                                                                                                                                                                                                                                       GLNGTARIASSPLASSPPLWLSRAP-PPSPPSGPETAEAAALFSRECRPSPAQL---GAL
                                                                                                                                                                                                                                                                                             ASLSAERCLAVCQPLRARRLLTPRRTCRLLSLVWVASLGLALPMAVIMGQKHE-----
                                                                                                                                                                                                                                                                                                                    TALSVERYLAICRELRARVLVTRRRVRALIAVLWAVALLSAGEFLFLVGVEQDEGISVVP 189
                                                                                                                                                                                                                                                                                                                                          RLRYHVLSLALSALLLLLISVPMELYNFVWSHYPWVFGDLGCRGYYFVRELCAYATVLSV 126
                                                                                                                                                                                                                                                                                                                                                                 TTNLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTYATLLHM 129
                                                                                                                                                                                                      RSPLWELTAILNGITVNHLVALYSQVPSASAQVNSIPSRLELLSEEGLLGFITWRKTLSL
                                                                                                                                                                                                                                                                                                                                                                                        WPPRPSPSAGLSLEARLGVDTRLWAKVLFTALYSLIFALGTAGNALSVHVVLKARTGRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR01479; NEUROTENSINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS00237; G_PROTEIN_RECEP_F1_2; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
n coupled receptor; Transmembrane; Lipoprotein;
1 32 EXTRACELLULAR (POTENTIAL).
 receptor
          (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
65
68
110
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177
108
                                                         STANDARD;
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176
217
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type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.7%;
                                                                                                                                                                                                                                                  -MERADGEPEPAS----RVCTVLVSRASSRSTFQVKRAGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Mismatches 146; Indels
(NT-R-2) (High-affinity levocabastine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 404;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY PALMITATE (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (POTENTIAL)
CYTOPLASMIC (F
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CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
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                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EBFDDBD6507223DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                        416 AA
           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palmitate.
                                                                                                                                    383
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                                                                                                                                                                                                                            281
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Best Local Sim
Matches 122;
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R PRINTS; PRO1479; NEUROTENSINR.

R PRINTS; PRO1479; NEUROTENSINR.

R PROSITE; PSO1237; G_PROTEIN RECEP F1 2; 1.

R PROSITE; PSO1237; G_PROTEIN RECEP F1 2; 1.

R PROSITE; PSO1262; G.PROTEIN A.

R PROSITE; PSO1262; G.PROTEIN A.

R PROSITE; PSO1262; G.PROTEIN A.

R PROSITE; PSO1262; G.PROTEIN A.

R PROSITE; PSO1262; G.PROTEIN A.

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R PROSITE; PSO1262; G.PROTEIN A.

R PROSITE; PSO1262; G.PROTEIN A.

R PROSITE; PSO12622; G.PROTEIN A.

R PROSITE; PSO12622; G.PROTEIN A.

R PROSITE; PSO12622; G.PROTEIN A.

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R PROSITE; PSO12622; G.PROTEIN A.

R PROSITE; PSO12622; G.PROTEIN A.

R PROSITE; PSO126222; G.PROTEIN A.

R PROSITE PSO12622; G.PROTEIN A.

R PROSITE; PSO126222; G.PROTEIN A.

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LIPID
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96228041; PubMed=8647296;
Chalon P., Vita N., Kaghad M., Guillemont M., Bonin J.,
Delpech B., le Fur G., Ferrara P., Caput D.;
"Molecular cloning of a levocabastine-sensitive neurotensin
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X97121; CAA65787.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTSR2 OR NTR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sensitive neurotensin receptor).
                                                      18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: ABUNDANT IN CORTEX AND HYPOTHALAMUS, AND LOWER LEVELS SEEN IN THE HEART AND INTESTINE.
DEVELOPMENTAL STAGE: EXPRESSED MAXIMALLY IN 7-DAY-OLD BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S Lett. 386:91-94(1996).
FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATED WITH G PROTEINS THAT ACTIVATE CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSION DECREASES PROGRESSIVELY UNTIL ADULTHOOD
                                              PWPALP-----PCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRT
  PWPPRPSPSAGLSLEARLGVDTRLWAKVLFTALYSLIFAFGTAGNALSVHVVLKARAGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00001;
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000276; GPCR_Rhodpsn.
IPR003986; NT2_rec.
IPR003984; NT_rec.
                                                                                                                                                                                                    416
                                                                                                    Conservative
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                                                                                                                                                                                                    46265 MW;
                                                                                                                      18.6%;
                                                                                             68;
                                                                                                                      Score 401;
Pred. No. 4
                                                                                                                                                                                                                      BY SIMILARITY PALMITATE (PO
                                                                                                                                                                                                                                                                            CYTOPLASMIC
                                                                                                                                                                                               ALMITATE (POTENTIAL).
127FC5F5CB6FE208 CRC64;
                                                                                               Mismatches
                                                                                                                      4.1e-19;
                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                               145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Þ
                                                                                                                                              Length 416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (35-DAY-OLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palmitate
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80
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                                                                                               Gaps
65
                                                                                               13;
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-TTNLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTYATLLH

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ESLGSLCGE
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R PROSITE; PS00237; GFCRRHODOPSN.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1_2; 1.

M Multigene family; Lipoprotein; Palmitaene; Glycoprotein; Palmitaene
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Best Local
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InterPro; IPR000276; GPCR_Rhodpsn.
SSR5_RAT
P30938;
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
BY SIMILARITY
V -> VV (IN REF. 1).
YGF -> LWL (IN REF. 2).
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Pred. No. 3.8
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N-LINKED (GLCNAC . .)
N-LINKED (GLCNAC . .)
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SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE=Liver;
MEDLINE=97/44289; PubMed=9300821;
Lublin A.L., Diehl N.L., Hochgeschwender U.;
"Isolation and characterization of the gene (Mus musculus) somatostatin receptor (msst5)
Gene 195:63-66(1997).
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baumeister H., Roosterman D., Schafer J., Kreuzer O., Meyerhof W.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases. Submitted (RECEPTOR FOR SOMATOSTATIN-28. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALEJC; TISSUE=Liver; STRAIN=BALEJC; TISSUE=Liver; Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Wood W.M., Knauf H., James Gordon D.F., Woodmansee W.W., Wood W.M., Wood W.M., Knauf H., James Gordon D.F., Woodman H., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., Wood W.M., W.M., Wood W.M., W.M., Wood W.M., W.M., Wood W.M., W.M., Wood W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M., W.M.,
entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                               http://www.isb-sib.ch/announce/
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EMBL; AF004740; AAB61418.1; -.
EMBL; AF030441; AAB6492.1; -.
EMBL; AF035777; AAB88302.1; ALT_INIT.
HSSP; P02699; 1F88.
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RESULT SSR5\_MOI

MOUSE

SSR5

MOUSE

STANDARD;

PRT;

OO8858; OO8998; Ol-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence up 15-JUL-1998 (Rel. 36, Last annotation Somatostatin receptor type 5 (SSSR).

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

musculus (Mouse)

NCBI\_TaxID=10090;

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342

186 180

235 289

ALYS-QVPSASAQVSSIPSRLELLSE----

129

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Moldovan S., Demayo F., Submitted (JUN-1997) to

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SEQUENCE FROM N.A.

STRAIN=129/SvJ; SEQUENCE FROM N.A. SEQUENCE FROM N.A.

STRAIN=129/SvJ;

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PARETTE R., Greenwood M.T., Warszynska A., Demchyshyn L.L., Day R., Wiznik H.B., Srikant C.B., Patel Y.C.;

If Miznik H.B., Srikant C.B., Patel Y.C.;

If "Molecular cloning, functional characterization, and chromosomal localization of a human somatostatin receptor (somatostatin receptor functional receptor somatostatin receptor functions, RECEPTOR FOR SOMATOSTATIN-28. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENVIYL CYCLASE.

INTESTINE LOCATION: Integral membrane protein.

INTESTINE LOW LEVELS IN ISLETS AND SPLEEN. NOT DETECTED IN KIDNEY, PANCREAS, CEREBELLUM, OR CORTEX.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                Pfam; PFO0001; TRN 11.

R Pfam; PF00001; 7cm [1 l. ]

R PFAM; PF00001; 7cm [1 l. ]

R PRINTS; PR00237; GPCREHODOPEN.

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EMBL; U01152; AAC09011.1; -.
EMBL; X74028; CAA52825.1; -.
HSSP; P02699; 1F88.
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01-FEB-1996
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                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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Last annotation update)
type 5 (SS5R).
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             CYTOPLASMIC (POTENTIAL).
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SIMILARITY
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            Clamp M.,
Bagguley C
Bird C.P.,
                                                                                                             Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M., Srikant C.B., Kent G., Patel Y.C., Niznik H.B.; "A human somatostatin receptor (SSTR3), located on chromosome 22, displays preferential affinity for somatostatin-14 like peptides."; FEBS Lett. 321:279-284(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSR3_HUMAN
P32745;
01-OCT-1993
                                                                      SEQUENCE FROM N.A. MEDLINE=20057165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                         Dunham
                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=93238970; PubMed=8097479;
                                                                                                                                                                                                                                                    adenylyl cyclase.
                                                                                                                                                                                                                                                                                        MEDLINE=93149123; PubMed=1337145;
Yamada Y., Reisine T., Law S.F., Ihara Y.,
Seino M., Seino Y., Bell G.I., Seino S.;
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              "Somatostatin receptors, an expanding functional characterization of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                   Endocrinol. 6:2136-2142(1992).
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y C., bc.
b., Blakey
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         0057165; PubMed=10591208;
, Hunt A.R., Collins J.E., Bruskiewich R., Beare Smink L.J., Ainscough R., Almeida J.P., Babbage C., Bailey J., Barlow K.F., Bates K.N., Beasley O, Blakey S.E., Bridgeman A.M., Buck D., Burgess J
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27.3%;
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; 4BD4512960613B4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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No. 2.1e-16;
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                                                                                                                                                                                                                                                               SSTR3,
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                                                                                                                                                                                                                                                                                                         Kubota A.,
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                                                                                                                                                                                                                                                                                                         Kagimoto
                       0.P.,
                                     A.K.,
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RA Clegg S.M., Cobley V.E., Cole C.G., Carter N.P., Chen Y., Clark G., RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., RA CONTON D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., RA Evans K.L., Rey J.M., Pleming K., French L., Garner A.A., RA Evans K.L., Fey J.M., Pleming K., French L., Garner A.A., RA Evans K.L., Goward M.E., Graffamm D.V., Griffiths M.N.D., Hall C., RA Hall R.E., Hall Tamhyn G., Heathcott R.W., Ho S., Holmes S., RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A., RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C.L., Lloyd D.M., RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., RA Scott C.E., Spragon L., Steward C.A., Sinston J.E., Smith M.L., Ross M.T., RA Scott C.E., Spragon L., Steward C.A., Sinston J.E., Swahn R.M., Ramsay H., Ramsey Y., Rogers L., Shimizu N., Williams C.L., Hubbard T. Bentley D.R., Beck S., Rogers L., Shimizu N., Williams C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., RA Wright C.L., Hubbard T., Bentley D.R., Deschamps S. Do A., Do T., RA Wright C.L., Hubbard T., Kansaki Y., Aoki N., Mitsuyama S., RA Wright C.L., Hubbard T., Kansaki Y., Aoki N., Mitsuyama S., RA Minoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J., Ra Ra Wright C.J., Williamson D., Benis G., Bentley D., Bradshaw H., Bourne S., RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Ra Ra Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Ra Mang Q., Wang Y., Mansley A., Wohldmann P., Pepin K., Nelson J., Ra Mang Q., Shakh T., Kurahashi H., Saitta S., Budarf M.L., Ra Ramuel B.S., Shakh T., Kurahashi H., Saitta S., Budarf M.L., Ra Ramuel B.S., Shakh T., Kurahashi H., Saitta S., Budarf M.L., Ra Ramuel B.S., Shakh T., Kurahashi H., Saitta S., Budarf M.L., Ra Ramuel S., La Raman L., Walson M., Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                               PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                    EMBL; M96738; AAA60592.1;
EMBL; Z82188; CAB45263.1;
PIR; S32501; S32501.
PIR; A46226; A46226.
                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                        Genew; HGNC:11332; SSTR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 COUPLED VIA PERTUSSIS TOXIN SENSITIVE G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADENYLYL CYCLASE.
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                             IPR000276; GPCR_Rhodpsn
                                                                                                            Polymorphism
CYTOPLASMIC (PO
2 (POTENTIAL).
EXTRACELLULAR
                                                                 EXTRACELLULAR (POTENTIAL)
1 (POTENTIAL).
                                               (POTENTIAL).
    (POTENTIAL)
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Best Local
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CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                          043194;
043194;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
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                       MEDLINE=98110578; PubMed=9441746; McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D., Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.; "Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                          GP39
                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
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                                                                                                                                             'ISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTASPSVTNVYILNLALADELFMLGLPF-LAAQNALSYWPFGSLMCRLVMAVDGINQFTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENA-SSAWPPDATLGNVSAGPSPAGLAVSGVLIPLVYLVVC--VVGLLGNSLVIYVVLR
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Primates;
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Pred. No. 2.9
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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CYTOPLASMIC
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1227095F801190C4 CRC64;
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                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                      Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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204 245 184

321

130

71 65

9;

TRANSMEM DOMAIN

DOMAIN

43 69 79 101 116

Multigene

MIM; 182453;

InterPro;

PF00001; 7tm

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Query Match
Best Local Similarity
Matches 111; Conserv
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SEQUENCE
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DOMAIN
TRANSMEM
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Pfam; PF000001; 7tm 1; 1.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G PROTEIN TRANSMEMBYANE;
PXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 46:426-434(1997).
-!- SUBCELLUTLAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
344 YTVSSQQFRRVFVQVLCCRLSLQHANHEKR 373
                                 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                               224 IFGAFVVYLVVLLSVAFMCWNMMQVLMKSQKGSLAGGTRPPQLRKSESEESRTARRQTII
                                                                                                                                                                                                 180 LVN-VPSHRGLTCNRSSTRHHEQ------PETSNMSICTNLSSRWTVFQSS
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                                                                                             VLLVVVLAFIICWLÞFHVGRIIYI--NTEDSRMYFSQYFNIVALQ--LFYLSASINPIL 354
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                              YNLISKKYRAAAFKLLLARKSRPRGFHRSR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                         PALPPCDERRCS-----PFPLGALVPVT--AVCLCLFVVGVSGNVVTV---MLIGR 65
                                                              FLRLIVVTLAVCWMPNQIRRIMAAAKPKHDWTRSYFRAYMILLPFSETFFYLSSVINPLL
                                                                                                                                                                                                                                                                                        ATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDP 183
                                                                                                                                                                                                                                                                                                                                     KGYLQKEVTDHMVSLACSDILVFLIGMPMEFYSIIWNPLTTSSYTLSCKLHTFLFEACSY 120
                                                                                                                                                                                                                                                                                                                                                                                                       PSLPGSD----CSQIIDHSHVPEFEVATWIKITLILVYLIIFVMGLLGNSATIRVTQVLQK 60
                                                                                                                                                                 -LGALRYMLWYTTAYFFLPFLCLSILYGLIGRELWSSRRP--LRGPAASGRERGHROTKR 298
                                                                                                                                                                                                                                                                      ATLLHVLTLSFERYIAICHPFRYKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTEY-P 179
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
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PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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318.5 14.8 387 2 JC5949 318 14.7 380 2 J138435 angiotensin receptor 2 317 14.7 398 1 JQ1059 317 14.7 411 2 I56444 thyrotrophin-releas 317 14.7 411 2 S23436 thyrotrophin-releas 318 14.6 391 2 C41795 319 14.4 373 2 JC0087 delta opioid receptor 2 311 14.4 373 2 JC0087 neurokinin z receptor 311 14.4 373 2 JC0087 neurokinin z receptor 311 14.4 373 2 JC0516 neurokinin z receptor 311 14.4 373 2 JC0516 neurokinin z receptor 311 14.4 373 2 JC0516 neurokinin z receptor 311 14.4 391 2 JC0516 neurokinin z receptor 308.5 14.3 392 2 S65693 meurokinin z receptor 308.5 14.3 392 2 S65693 mu opiate receptor 308.5 14.3 392 2 JC56517 mu opioid receptor 308.5 14.3 392 2 JC5653 mu opioid receptor 308.5 14.3 398 2 JC5653 mu opioid receptor 308.5 14.3 309 2 JC5653 mu opioid receptor 308.5 14.3 309 2 JC5653 mu opioid receptor 308.5 14.3 309 2 JC5653 mu opioid receptor 308.5 14.3 309 2 JC5653 mu op	45	44	43	42	41	40	39	38	37	36	35	34	33	32	ω L	30
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	somatosta	mu opioid	somatostatin recep	mu opiate receptor	opioid receptor mu	somatostatin	somatostatin	neurokinin	delta opioid	somatostatin	thyrotropin-releas	thyrolibe	thyrotrophin-relea	neurokinin 2	angiotensin recept	galanin receptor

# ALIGNMENTS

neurotensin receptor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1991 #sequence\_revision 31 C;Accession: JH0164 R;Tanaka, K.; Masu, M.; Nakanishi, S.

31-Dec-1991 #text\_change 17-Mar-2000

rat neurotensin receptor

R;Tanaka, K.; Masu, M.; Nakanishi, S. Neuron 4, 847-854, 1990 A;Tille: Structure and functional expression of the cloned A;Reference number: JH0164; MUID:90297956; PMID:1694443

A; Accession: JH0164

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A; Molecule type: mRNA
A; Residues: 1-424 <TAN>
C; Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The comment: Neurotensin receptor and as a hormone) cellular mediator in peripheral tis C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F; 65-87/Domain: transmembrane #status predicted <TM3>
F; 121/Domain: transmembrane #status predicted <TM4>
F; 144-165/Domain: transmembrane #status predicted <TM4>
F; 189-210/Domain: transmembrane #status predicted <TM4>
F; 189-210/Domain: transmembrane #status predicted <TM5>
F; 199-330/Domain: transmembrane #status predicted <TM6>
F; 348-372/Domain: transmembrane #status predic
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310 CWLPFHVGRIIYINTEDSR----MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAA 365
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Gaps

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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo: A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www_sanger.ac.uk/Projects/C_ele_1,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: A88013
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                       protein K10B4.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, FEBS Lett. 317, 139-142, 1993
A;Title: Cloning and expression of a complementary DNA encoding a high affinity A;Reference number: S29506; MUID:93154505; PMID:8381365
A;Accession: S29506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
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                                                                                                                                                                         R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFKLLLARKSRPRGFHRSRDT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRLMFCYISDEQWTPFLYDFYHYFYMVTNALFYVSSTINPILYNLVSANFRHIFLATLAC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLTVMVRQAAEQGQVCTVGGEHSTFSMAIEPGRVQALRHGVRVLRAVVIAFVVCWLPYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELWSSRRPL--RGPAAS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RSADGQHAGGLVCTPT-IHTATVKVVIQVNTFMSFIFPMVVISVLNTIIAN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTKKFISAIWLASALLTVPMLFTMG-EQN--
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                                                                                                                                                                                                                                                                                                                                                       A;Cross references: GB:X97121; NID:g1483579; PIDN:CAA65787.1;
A;Experimental source: hypothalamus
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
F;33-58/Domain: transmembrane #status predicted <TM1>
F;70-91/Domain: transmembrane #status predicted <TM2>
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A; Map position:
                                                                                                                                                                                                                                                        F;110-131/Domain: transmembrane #status predicted <TM3>F;155-175/Domain: transmembrane #status predicted <TM4>F;204-230/Domain: transmembrane #status predicted <TM5>F;296-315/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Chalon, P.; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpech, B.; FEBS Lett. 386, 91-94, 1996
A;Title: Molecular cloning of a levocabastine-sensitive neurotensin binding A;Reference number: S68822; MUID:96228041; PMID:8647296
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A; Residues: 1-416 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1997 #sequence_revision 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurotensin receptor 2, levocabastine-sensitive - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S68822
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                                      PWPPRPSPSAGLSLEARLGVDTRLWAKVLFTALYSLIFAFGTAGNALSVHVVLKARAGRP 65
                                                                                       PWPALP----PCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRT 71
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Pred. No. 1.6e-27;
                                                                                                                                                    Score 401; DD -. No. 7.5e-25;
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_of;Accession: T15816
R;Favello, A.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C48C5.
A;Reference number: Z18410
A;Accession: T15816
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roeiduse: 1-378 <FAV>
A;Cross references: EMBL: U39994; NID:g1055102; PID:g105510
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A;Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1;
C;Superfamily: adenosine receptor Al
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A;Experimental source: strain Bristol N2; clone C48C5
C;Genetics:
A;Gene: CESP:C48C5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 LVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLIL-LGLPFDLY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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QYFNIVALQLFYLSASINFILYNLISKKYRAAAFKLLL 371
                                                                       -SSNRTIQPGELDITEELQMRINAILCAIVSAFFICYLPFQLQRLLFFYFDNEVILTWVN 319
                                                                                                                    WSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDSRMM-YFS 333
                                                                                                                                                                                                                  PSPPSGPETAEAAALFSRECRPSPAQLGALRVML-WVTTAYFFLPFLCLSILYGLIGREL 274
                                                                                                                                                                                                                                                              GTIIGFTWIFSILCAMP--FAIHHRADYIMKSWPGTDNRIPVKSSKMCM-------
                                                                                                                                                                                                                                                                                                          RALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPP 215
                                                                                                                                                                                                                                                                                                                                                                                                        RLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPL-RARVLVTRRRV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYKVTALYIFIFLVGVIGNTTTCLVMKKHPMMKTHASMYLMNLAVSDLVTLCVGLPFEVM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHKDASQIRSLQHSAQVLRAIVAVYVICWLPYHARRLMYCYIPDDGWTNELYDFYHYFYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RERGHROTK-----RVLLVVVLAFIICWLPFHVGRIIYINTED----SRMMYFSQYFNI 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALYS-QVPSASAQVSSIPSRLELLSE------EGLLGFITWRKTLSLGVQASLV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPEPASRVCTVLVSRATLQVFIQVNVLVSFALPLALTAFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQDPGISVVPGLNGTARIA------SSPLASSPPLWLSRAPPPSPPSGPETAEAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VASLSAERCLAVCQPLRARRILTPRRTRRLLSLVWVASLGLALPMAVIMGQKHEVESADG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGV----- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRIRYHVISIALSALLLLLVSMPMELYNFVWSHYPWVFGDIGCRGYYFVREICAYATVIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TTNLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTYATLLH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                   -IAVMF-----EPKLASTFKILFHFSAIAFFALPLFTIVILYARIACKV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.5%; Score 378; DB 2; 28.7%; Pred. No. 4.9e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NGITVNHLM 234
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C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: pituitary R;Penetta, R.; Greenwood, M.; Patel, Y.C. submitted to the EMBL Data Library, August 1993 A;Description: Correction of the nucleotide and A;Reference number: S39244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L04535; NID:g409238; PIDN:AAA17029.1; R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C. Mol. Pharmacol. 44, 1278, 1993
A;Title: Molecular cloning and expression of a pituitary soma A;Reference number: I57949; MUID:94088493; PMID:8264565
A;Accession: I57949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999 (c;Accession: I57940; I57949; Is 193244 R;O'Carroll, A.M.; Loclait, S.J.; Konig, M.; Mahan, L.C. Mol. Pharmacol. 42, 939-946, 1992 Mol. Pharmacol. 42, 939-946, 1992 A;Title: Molecular cloning and expression of a pituitary somatostatin recept A;Reference number: I57940; MUID:93125499; PMID:1362243 A;Accession: I57940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 341-363 <OCA2>
A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1;
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A; Residues: 309-363 < PEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S39244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-363 <OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: somatotropin release-inhibiting factor subtype 28 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     somatostatin receptor 5 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I57940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                        303
                                                                     354 LYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGG 396
                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 QYMYFISGFLFYLATIINPIAYNLASSRFR-RAFKDIL 356
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                                                                                                                                                                                                                                                                                                                                                       DPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQ 241
                      LYGFLSDNFROSFRKVLCLR----RGYGMEDADAIEPRPDKSG
                                                                                                                 KVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGLYFFVVVLS--YANSCANPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNASAASSGNHN--WSLVG-----SASPMGÄRAVLVPVLYLLVC--TVGLSGNTLVIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNGSDGPEGAREPPWPALPPCDERRCSPFPLGA---LVPVTAVCLCLFVVGVSGNVVTVM 61
                                                                                                                                                              QTKRVLLVVVLAFIICWLPFHVGRIIYIN-TEDSRMMYFSQYFNIVALQLFYLSASINPI 353
                                                                                                                                                                                                          LWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR------
                                                                                                                                                                                                                                                    LGALRVMLWVTTAYFFLPFLCLSILYGLI------GRELWSSRRPLRGPAASGRERGHR 294
                                                                                                                                                                                                                                                                                                                                                                                                 QFTSIFCLMVMSVDRYLAVVHPLRSARWRRPRVAKMASAAVWVFSLLMSLPLLVFADVQE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVLRHAKMKTVTNVYILNLAVADVLFMLGLPFLATQNAVVSYWPFGSFLCRLVMTLDGIN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-363 <OCA1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 358; DB 2;
Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 149; Indels
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                                                                                                                                                                                                             -RRRSEP
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12;

somatostatin receptor 3 -

human

Accession: A46226; S32501

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365 AAFKLLLARKSR 376

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F;289-316/Domain: transmembrane """ (covalent, """" F;189-316/Domain: transmembrane (Asn) (covalent, """" F;17,30/Binding site: carbohydrate (Asn) (covalent) (by protein kinase C) #status F;116-191/Disulfide bonds: #status predicted F;116-191/Disulfide bonds: #status predicted F;151,251,317,332/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;251/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F;251/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, FEBS Lett. 321, 279-284, 1993
A;Title: A human somatostatin receptor (SSTR3), located A;Reference number: S32501; MUID:93238970; PMID:8097479
A;Accession: S32501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M96738; NID:g338498; PIDN:AAA60592.1; PID:g338499
A;Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)
R;Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Somatostatin receptors, an expanding gene family: cloning and functional A;Reference number: A46226; MUID:93149123; PMID:1337145
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;Date: 21-Sep.1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
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ol. Endocrinol. 6, 2136-2142, 1992
                              265 LFVLCWMPFYVLNIVNVVCPLPEEPAFFGLYFLVVALP--YANSCANPILYGFLSYRFK-
                                                                                                        AFIICWLPFHVGRIIYINTE-DSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRA 364
                                                                                                                                                                                                                                                                                  RVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVLLVVVL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGAL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTASPSVTNVYILNLALADELFMLGLPF-LAAQNALSYWPFGSLMCRLVMAVDGINQFTS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYAT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEGAREPPWPALPPCDERRCSPFPL----GALVPVTAVCLCLFVVGVSGNVVTVMLIGR 65
                                                                                                                                                                                                   GFIIYTAALGFFGPLLVICLCYLLIVVKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVWVASAVVVLPVVVFSGV-----
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                                                                                                                                                                                                                                                                                                                                                                     ------PRGMSTCHMQ------WPEPAAAWRA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 418;
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A;Title: Molecular cloning, functional characterization, A;Reference number: 157955; MUID:94195267; PMID:7908405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                somatostatin receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999 C;Accession: I57955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchyshyn, L.L.; Day, R.; Niznik,
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                                                                                                                                               R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; l Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization A;Reference number: JN0762; MUID:93384611; PMID:8373420
                                                                                                                                                                                                                                                                                                                                                                somatostatin receptor 5 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
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C; Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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                                       A; Molecule type: DNA
A; Residues: 1-364 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JN0763
                                                                                                                         A; Accession: JN0763
                                                                                                                                                                                                                                                                                                                                  C; Accession: JN0763
A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRMVLVVVLVFAGCWLPFFTVNIVNLAVALPQEPASAGLYF---FVVI---LSYANSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGAVFIIYTAVLGFFAPLLVICLCYLLIVVKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLRFAKMKTVTNIYILNLAVADVLYMLGLPF-LATQNAASFWPFGPVLCRLVMTLDGVNQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTPSWNASSPGAASGGGDNRTLVGPAPSAGARAVLVPVLYLLVC--AAGLGGNTLVIYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLASAAAWVLSLCMSLPLLVFADVQE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVLYGFLSDNFRQSFQKVLCLRK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILYNLISKKYRAAAFKLLLARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106;
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DDBJ:D16827; NID:g487683; PIDN:BAA04107.1; PID:g487684
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                                                                                                                                                                                                                                                                                                   Someya, Y.; Ihara, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PEPVGL
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A;Introns: #status absent C;Superfamily: vertebrate rhodopsin

A,Cross-references: GDB:134187; OMIM:182453 A,Map position: 22q13.1-22q13.1

A;Gene: GDB:SSTR3

Genetics:

A; Status: preliminary

A;Residues: 1-418 <YAM> A;Molecule type: DNA A;Accession: A46226

A;Residues: 1-418 <COR> A; Molecule type: DNA

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Query Match Best Local Similarity

16.5%;

Score 356.5; Pred. No. 3e-Mismatches

3e-21;

Matches

100;

Conservative

63;

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A;Map position: 16p13.3-16p13.3

A;Introns: #status absent

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thic

F;40-66/Domain: transmembrane #status predicted <TM1>
F;17-102/Domain: transmembrane #status predicted <TM3>
F;114-135/Domain: transmembrane #status predicted <TM4>
F;114-135/Domain: transmembrane #status predicted <TM5>
F;145-17/Domain: transmembrane #status predicted <TM6>
F;260-207/Domain: transmembrane #status predicted <TM7>
F;30-28/Domain: transmembrane #status predicted <TM7>
F;246-277/Domain: transmembrane #status predicted <TM7>
F;280-307/Domain: transmembrane #status predicted <TM7>
F;30,26,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F;247/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
F;320/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                        R;Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
A;Title: Primary structure and functional expression of a guinea pig kappa opioid (dynor A;Reference number: A55259; MUID:94224825; PMID:8170987
A;Accession: A55259
                                                                                                                                                                                                                                                                                                                                    kappa opioid receptor - guinea pig
N;Alternate names: dynorphin receptor
C;Species: Cavia porcellus (guinea pig)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Nov-1999
      C; Superfami.
C; Keywords:
                                                       A; Cross-references: GB: U04092; NID: g476106; PIDN: AAA67171.1; PID: g476107
                                                                                        A; Molecule type: mRNA
A; Residues: 1-380 < XIE>
                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: SSTR5
Superfamily: vertebrate rhodopsin
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLYGFLSDNFRQSFQKVLCLRK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILYNLISKKYRAAAFKLLLARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRMVLVVVLVFAGCWLPFFTVNIVNLAVALPQEPASAGLYF---FVVI---LSYANSCAN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG-----RERGHRQT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YATLIHMTALSVERYLAICRPIRARVIVTRRRVRALIAVIWAVALISAGPFIFIVGVEQD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLRFAKMKTVTNIYILNLAVADVLYMLGLPF-LATQNAASFWPFGPVLCRLVMTLDGVNQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRVLLVVVLAFIICWLPFHVGRIIYI-----NTEDSRMMYFSQYFNIVALQLFYLSASIN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGAVFIIYTAVLGFFAPLLVICLCYLLIVVKV-----RAAGVRVGCVRRRSERKV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLASAAAWVLSLCMSLPLLVFADVQE- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASTPSWNASSPGAASGGGDNRTLVGPAPSAGARAVLVPVLYLLVC--AAGLGGNTLVIYV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;26-48/Domain: transmembrane #status predicted <TM1>
F;58-80/Domain: transmembrane #status predicted <TM2>
F;97-118/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 250, 68-71, 1998
A;Title: Cloning and characterization of a new subtype of thyrotropin-releasing hormone
A;Reference number: JE0296; MUID:98407892; PMID:9735333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thyrotropin releasing hormone receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                          F;282-304/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: adenosine receptor Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: DDBJ:AB015645; NID:g3660553; PIDN:BAA33437.1; PID:g3660554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-352 < ITA>
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                                                                                             150 VTRRVRALIAVLWAVALLSAGPFLFLVGV-----EQDPGISVVPGLNGTARIASSPLA 203
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                                                                                                                                                                                                                                                                                                                                                          Local
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SSPPLWLSRAPPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCL
                                              CTVARAKRITAGIWGVTSLYCLLWFFLVDLNVRDNQRLECGYKVPRGL------
                                                                                                                                            SL--VGHWIYGRAGCL-----GITYFQYLGINVSSFSILAFTVERYIAICHPLRAQTV 133
                                                                                                                                                                                     RLWRSRPWVFGPLLCRLSLYVGEGCTYATLL-----HMTALSVERYLAICRPLRARVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVGLVGNSLVMEVIIRYTKMKTATNIYIFNLALADALVTTTMPFQ-STVYLMNSWPFGDV 129
                                                                                                                                                                                                                                    VVSVFLVLLVCTLGIVGNAMVILVVLTSRDMHTPTNCYLVSLALADLLVLLAAGLPNVSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPL 109
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                                                                                                                                                                                                                                                                                                                                  108;
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                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                        Score 338; DB 2;
Pred. No. 7.7e-20;
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                                                                                                                                                                                                                                                                                                                                  109;
                                                                                                                                                                                                                                                                                                                                                                              Length 352;
                                                                                                                                                                                                                                                                                                                               Indels 106; Gaps
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Query Match  15.7%; Score 338; DB 2; Length 380;  Best Local Similarity 25.5%; Pred. No. 8.4e-20;  Matches 103; Conservative 75; Mismatches 146; Indels 80; Gaps 13;  Qy 6 NGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVML 62	ated from GB/EMBE/DUBD 42; NID:g403486; PIDN:AAA18261.1; dopsin receptor; transmembrane protein	Residues: 1-344,'Y',346-380 <lis> Cross-references: GB:L22536; NID:g42E Cross-references: GB:L22536; NID:g42E GEORGE, F.; Xie, GEORGE, F.; Axie, GEORGE, F.; Axie, GEORGE, F.; Axie, GEORGE, G</lis>	A; Molecule Type: mkNA  A; Residues: 1-41, 'L', 'A3-380 <min> A; Residues: 1-41, 'L', 'A3-380 <min> A; Cross-references: GB:D16829; NID:g404115; PIDN:BAA04109.1; PID:g404116 A; Cross-references: GB:D16829; NID:g404115; PIDN:BAA04109.1; PID:g404116 A; Cross-references: GB:D16829; NID:g404115; PIDN:BAA04109.1; PID:g404116 A; Cross-references: GB:D16829; NID:g404115; PIDN:BAA04109.1; PID:g404116 A; Title: Molecular cloning and expression of a rat kappa opioid receptor. A; Reference number: S39015; MUID:94059009; PMID:8240268 A; Accession: S39015 A; Accession: S39015</min></min>	A;Residues: 1-380 CCHE> A;Residues: 1-380 CCHE> A;Residues: 1-380 CCHE> A;Cross-references: GB:L22001; NID:g409236; PIDN:AAA41495.1; PID:g409237 A;Cross-references: GB:L22001; NID:g409236; PIDN:AAA41495.1; PID:g409237 R;Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S.; Sat FEBS Lett. 329, 291-295, 1993 A;Title: Cloning and expression of a cDNA for the rat kappa-opioid receptor. A;Reference number: S36102; MUID:93374033; PMID:8103466 A;Accession: S36102	A;Accession: 536143 A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-380 <nis> A;Cross-references: GB:D16534; NID:g409390; PIDN:BAA03971.1; PID:g415310 A;Cross-references: GB:D16534; NID:g409390; PIDN:BAA03971.1; PID:g415310 A;Chen, V; Mestek, A.; Liu, J.; Yu, L. Biochem. J. 295, 625-628, 1993 A;Title: Molecular cloning of a rat kappa opioid receptor reveals sequence similarities A;Reference number: S38825; MUID:94059008; PMID:8240267 A;Accession: S38825 A;Status: preliminary A;Molecular type: mRNA A;Molecular type: mRNA</nis>	RESULT 12 S36143 S36143 S36143 S36143 S36143 S36143 S36123 S36143 C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Dec-1993 #sequence revision 19-Oct-1995 #text_change 20-Jun-2000 C;Accession: S36143; S38825; S36102; S39015; A48789 R;Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K. FEBS Lett. 330, 77-80, 1993 A;Title: cDNA cloning and pharmacological characterization of an opioid receptor with hi A;Reference number: S36143; MUID:93380575; PMID:8396539	Db 182
tor preferentially binds dynorphins.  DB:132651; OMIM:165196	bmitted to the EMBL Data Library, November 1 Reference number: G07718 Recession: G01546 Status: translated from GB/EMBL/DDBJ Molecule type: DNA Residues: 132-203 <gra> Residues: 132-203 <gra></gra></gra>	Cioning of a numen .kappa. Opioid receptor from cice number: 157005  on: 157005  preliminary; translated from GB/EMBL/DDBJ  Le type: mRNA Le type: mRNA List in item in the interval in the in	A;Reference number: A55354; MUID:95014415; PMID:7929306 A;Recession: A55354 A;Status: preliminary A;Molecule type: mRNA A;Residues: 136-279 <wan> A;Cross-references: GB:L36130; NID:9598184; PIDN:AAA63646.1; PID:g598185 A;Cross-references: GB:L36130; NID:g598184; PIDN:AAA63646.1; PID:g598185</wan>	A,Accession: JC2338 A,Molecule type: mRNA A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <man> A,Residues: 1-380 <min 1-380="" 1-380<="" <min="" a,residues:="" td=""><td>3 s: Hoid s: Ho 20-Fo 100: Biol 180 180</td><td>230 303 279 361</td><td>Db 39 NGSVGSEDQQLEPAHISBAIPVIITAVYSVVFVVGLVGNSLVMFV 83  Qy 63 IGRYRDMRTTINLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVPGPLLCRLSLYVGEGCT 122  QY 64 IIRYTKMKTATNIXIFNLALADALVTTIMPFQ-SAVYLMYSWPPGDVLCKLVISIDYYNM 142  QY 123 YATLLHMTALSVERYLAICRPLRARVLVTRRRVALIAVALLSAGPFLLVGVEQD 182  i : : :                                </td></min></man></man></man></man></man></man></man></man></man>	3 s: Hoid s: Ho 20-Fo 100: Biol 180 180	230 303 279 361	Db 39 NGSVGSEDQQLEPAHISBAIPVIITAVYSVVFVVGLVGNSLVMFV 83  Qy 63 IGRYRDMRTTINLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVPGPLLCRLSLYVGEGCT 122  QY 64 IIRYTKMKTATNIXIFNLALADALVTTIMPFQ-SAVYLMYSWPPGDVLCKLVISIDYYNM 142  QY 123 YATLLHMTALSVERYLAICRPLRARVLVTRRRVALIAVALLSAGPFLLVGVEQD 182  i : : :

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Somatostatin receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: J00605; J00762; A47457
R;Xu, Y:; Song, J:; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652; 1993
A;Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A;Reference number: J00605; MUID:93290656; pMID:8512564
A;Accession: J00605
A;Accession: J00605
A;Accession: J00605; MUID:93290656; pMID:8512564
A;Accession: J00605
A;Accession: J00605; MUID:93290656; pMID:8512564
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A;Accession: J00762; MUID:9328856; pMID:8A89934
A;Accession: J00762; MUID:9328856; pMID:8489934
A;Accession: J00762; MUID:9328856; pMID:8489934
A;Accession: J00762; MUID:9328856; pMID:8489934
A;Accession: J00762; MUID:9328856; pMID:8489934
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A;Accession: J00762; MUID:9328856; pMID:8489934
A;Accession: J00762; MUID:9328856; pMID:8489934
A;Accession: J00762; MUID
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C;Superfamily: vertebrate rhodopsin
C;Kuperfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; receptor; transmembrane
F;60-85/Domain: transmembrane #status predicted <TM1>
F;95-114/Domain: transmembrane #status predicted <TM2>
F;133-154/Domain: transmembrane #status predicted <TM4>
F;177-199/Domain: transmembrane #status predicted <TM4>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Someya, Y.; Ihara, Y.;
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A; Molecule type: mRNA
A; Residues: 1-367 < RES>
                                                                                                                                                       A;Reference number: I49022; MUID:95327076; PMID:7603458
A;Accession: I49022
                                                                                                                                                                                                       R;Pan, Y.X.; Cheng, J.; Xu, J.; Rossi, G.; Jacobson, E.; Ryan-Moro, J.; Brooks, A.I.; Mol. Pharmacol. 47, 1180-1188, 1995
A;Title: Cloning and functional characterization through antisense mapping of a kappa
                                                                                                                                                                                                                                                                                                  kappa opioid receptor 3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-7ul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000
C;Accession: I49022
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149022
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F;162-184/Domain: transmembrane #status predicted <TM4>
F;162-184/Domain: transmembrane #status predicted <TM5>
F;208-238/Domain: transmembrane #status predicted <TM5>
F;257-284/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;119-198/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status F;327/Binding site: palmitate (Cys) (covalent) #status predicted
C; Superfamily: vertebrate rhodopsin
                               A; Cross-references: EMBL: U09421; NID: g551484; PIDN: AAA81333.1;
                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: #status absent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRI--IYINTEDSRMMYFSQYFNIVALQL 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIFADTR-----SAVF-- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RSEKKITRLVLMVVVVFVLCWMPFYVVQLLNLVVTSLDATV-
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26.9%; Pred. No. 1.8e-19;
tive 65; Mismatches 128;
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                          199 VEIPAPODYWGPVFAICIFLFS--------FIIPVLIISVCYSLM 235
                                                                                                                                                                                                                                                                                                                160 TSSKAQAVNVAIWALASV-----L 198
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                                                                                                                          289 PGSE--TAVAILRECTALGYVNSCLNPILYAFLDENFKACFRKFCCA----SALHREMQ 341
                                                                                                                                                       331 YFSQYENIVALQLF----YLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRS-- 383
                                                                                                                                                                                       236 IRRL-RGVRLLSG--SREKDRNIRRITRLVIVVVANFVGCWTPVQV----FVLVQGLGVQ 288
                                                                                                                                                                                                                 271 GRELWSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHYGRIIYINTEDSRMM 330
                                                                                                                                                                                                                                                                            211 SRAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLI 270
                                                               342 VSDRVRTVAKDVG 354
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Result
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1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
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        GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                     0 US-09-825-294-209

0 US-09-966-871-77

2 US-10-039-645-77

0 US-09-966-871-76

2 US-10-039-645-76

0 US-09-823-114-23

US-10-087-345A-15

US-09-992-331-16

US-09-992-331-16

US-09-966-782A-16

US-09-966-782A-16
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US-09-992-331-14

US-09-992-331-17

US-09-966-782A-13

US-09-970-966-209
US-09-966-871-80
US-10-039-645-80
US-09-992-331-15
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                                                                                           Sequence 26, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 209, App
Sequence 209, App
Sequence 77, Appl
Sequence 77, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 80, 1
Sequence 80, 1
Sequence 15, Ap
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Sequence 16,
Sequence 16,
Sequence 9, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: DE 100 13 618.4
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Receptors for peptides from insects
FILE REFERENCE: Le A 394
CURRENT APPLICATION NUMBER: US/09/804,551B
CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 419
TYPE: PRT
ORGANISM: Drosophila melanogaster
170
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                                                                                                                                                             HPFLGQAMSKLSRAIRIIVLVWIMAĮVTAIPQAAQFGIEHYSGVE---
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                                                                       -----QCGIVRVIVKHSFQLSTFIFF 190
                                                                                                                  LASSPPLWLSRAPPPSSPPSGPETAEAAALFSRECRPSPAQLGALRVML----WVTTAYFF 257
                                                                                                                                                                                                                                                     SDFLLLLSGVPQEVSYIWSKYPYVFGEYICIGRGLLAETSANATVLTITAFTVERYIAIC 124
                                                                                                                                                                                                                                                                                                SDLLILL-GLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAIC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Mismatches 119; Indels 130;
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368 SKGSLNSRN 376

PRGFHRSRD 385

US-09-992-331-13

Sequence 13, Ap Publication No. GENERAL INFORMATION:

APPLICANT:

RAMANATHAN, CHANE HAWKEN, DONALD R. MINTIER, GABE

APPLICANT: FEDER, APPLICANT: MINTI

JOHN N.

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FILE REFERENCE: D0040NBE
CURRENT APPLICATION NUBER: US/09/992,331
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/308,540
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/248,483
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-01-16
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354 LYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGG 396
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                                                                                                                                                                                                                                                                                                                                                         QFTSIFCLMVMSVDRYLAVVHPLRSARWRRPRVAKLASAAVWVFSLLMSLPLLVFADVQE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGC 121
                                                     KVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGLYFFVVVLS--YANSCANPL
                                                                                                   QTKRVLLVVVLAFIICWLPFHVGRIIYIN-TEDSRMMYFSQYFNIVALQLFYLSASINPI 353
                                                                                                                                                         LWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR---
                                                                                                                                                                                                                                                                                                              DPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQ 241
                                                                                                                                                                                                                                                                                                                                                                                                               TYATLIHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVLRYAKWKTVTNVYILNLAVADVLFMLGLPF-LATQNAVSYWPFGSFLCRLVMTLDGIN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNASAASSGSHN--WSLVDPVS-----PMGARAVLVPVLYLLVC--TVGLGGNTLVIY 60
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                                                                                                                                                                                                       LGALRVMLWVTTAYFFLPFLCLSILYGLI-----GRELWSSRRPLRGPAASGRERGHR 294
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; TYPB: PRT
; ORGANISM: Rattus norvegicus
US-09-992-331-14
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PRIOR APPLICATION NUMBER: 05/09/992,331
CURRENT FILING DATE: 2001-01-07
PRIOR APPLICATION NUMBER: 60/308,540
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/261,782
PRIOR APPLICATION NUMBER: 60/261,782
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 45
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Publication No. US20030022186A1
                                                        Sequence 17, Application US/09992331 Publication No. US20030022186A1 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRHMY18,
TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
TITLE OF INVENTION: CELLS
FILE REFERENCE: DOOG 8 NP
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APPLICANT: MINTIER, GABE
APPLICANT: RAMANATHAN, C
APPLICANT: HAWKEN, DONAL
          APPLICANT: FEDER, JC APPLICANT: MINTIER,
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                                                                                                                                                                                                                                                                                                                                              KVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGLYFFVVVLS--YANSCANPL
                                                                                                                                                                                                                                          LYGFLSDNFRQSFRKVLCLR----RGYGMEDADAIEPRPDKSG
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                                     JOHN N
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27.3%; Pred. No. 8.8e-22;
tive 60; Mismatches 149;
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US-09-992-331-13

ORGANISM: Mus musculus

TYPE: PRT

Matches 112; Query Match Best Local

Conservative

Local Similarity

SOFTWARE: Pate SEQ ID NO 13 LENGTH: 362

PatentIn Ver. 2.1

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Sequence 13, Application US/09966782A
Publication No. US20030022183A1
GENERAL INFORMATION:
APPLICANT: Battaglino, P.
APPLICANT: Feder, J. N.
APPLICANT: Mintier, G.
APPLICANT: Westphal, R.
APPLICANT: Hawken, D. R.
APPLICANT: Hawken, D. R.
APPLICANT: Cacace, A.
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US-09-966-782A-13
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Best Local
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                      APPLICANT: Westphal, R.
APPLICANT: Hawken, D. R.
APPLICANT: Cacace, A.
APPLICANT: Barber, L.
APPLICANT: Borber, L.
APPLICANT: Kornacker, M. G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY7,
TITLE OF INVENTION: EXPRESSED HIGHLY IN SPINAL CORD
FILE REFERENCE: D0044NP
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PRIOR FILLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/248,483
PRIOR FILLING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 45
CURRENT APPLICATION NUMBER: US/09/966,782A
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/308,540
PRIOR FILING DATE: 2001-07-27
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APPLICANT: HAWKEN, DONALD R.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18,
TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
TITLE OF INVENTION: CELLS
FILE REFERENCE: D0048NP
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AAFKLLLARKSR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 AFIICWLPFHYGRIIYINTE-DSRMMYFSQYFNIYALQLFYLSASINPILYNLISKKYRA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 IFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVWVASAVVVLPVVVFSGV----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 GFIIYTAALGFFGPLLVICLCYLLIVVKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 RVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVLLVVVL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 LLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 HTASPSVTNVYILNLALADELFMLGLPF-LAAQNALSYWPFGSLMCRLVMAVDGINQFTS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 16.5%; Score 356.5; DB 9; Local Similarity 26.9%; Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFVLCWMPFYVLNIVNVVCPLPEEPAFFGLYFLVVALP--YANSCANPILYGFLSYRFK- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQLGAL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PRGMSTCHMQ-----WPEPAAAWRA 204
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PRIOR APPLICATION NUMBER: 60/235,731
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/268,580
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/315,423
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 64
  Query Match
Best Local Similarity
Matches 111; Conserv
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SEQ ID NO 209
LENGTH: 453
TYPE: PRT
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SEQ ID NO 13
SEQ ID NO 13
TYPE: PAT
ORGANISM: RAT
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Molesh, David Ala
APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stolk,
                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 SPLASSPPLWLSRAPPPSSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 VRHPLRSRALRTPRNARAAVGLVWLLAALFSAPYL-----SYYGTVRYGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 ICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIAS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 -LILIGLPFD--LYRLWRSRPWVFGPLLCR---LSLYVGEGCTYATLLHMTALSVERYLA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 SPFPLGALVPVTAVCLCLFVVGVSGN--VVTVML---IGRYRDMRTTTNLYLGSMAVSDL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGFHRSRDTAGEVAGDTGGDTVGY 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVVSLAYGRTLCFLWAAVGPAGAAAAEARRRATGRAGRAMLVVVVVVFGISWLPHHV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IHLWAEFGAFFLTPASFFFRITAHCLAYSNSSLNPLVYSLASRHFRARFRRLWPCGRRRH 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 David Alan
16.2%; Score 349.5; DB 9; 28.5%; Pred. No. 5.7e-21; tive 64; Mismatches 170;
                                                  Length 453;
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Conservative

45;

Gaps

13

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APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEO ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
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242 -LGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRP--LRGPAASGRERGHRQTKR 298
                                                                                                                                                                                                                                                                                                                                                                                                 20 PALPPCDERRCS-----PFPLGALVPVT--AVCLCLFVVGVSGNVVTV---MLIGR 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDP 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRP--LRGPAASGRERGHRQTKR 298
                                                                                             GISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPAQ-- 241
                                                                                                                                                  ATLLHVLTLSFERYIAICHPFRYKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTEY-P 179
                                                                                                                                                                                         ATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDP 183
                                                                                                                                                                                                                                               KGYLQKEVTDHMVSLACSDILVFLIGMPMEFYSIIWNPLTTSSYTLSCKLHTFLFEACSY 120
                                                                                                                                                                                                                                                                                                 YRDMRTTTNLYLGSMAVSDLLI-LLGLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTY 123
                                                                                                                                                                                                                                                                                                                                                PSLPGSD----CSQIIDHSHVPEFEVATWIKITLILVYLIIFVMGLLGNSATIRVTQVLQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 349.5; DB 10; Length 453; 28.5%; Pred. No. 5.7e-21; ative 64; Mismatches 170; Indels 45;
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/236,302
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/288,644
PRIOR APPLICATION NUMBER: US 60/288,644
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
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US-10-039-645-77
Sequence 77, Application US/10039645
Patent No. US20020147170A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kopin, Alan S.

TITLE OF INVENTION: Assays for Identifying Receptors
TITLE OF INVENTION: Alterations in Signaling
FILE REFERENCE: 00398/512002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 380
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                                                                                                                                                                            336 NFKRCFRDFCFPIKMRMERQST----NRVRNTVQDPASMRDVGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YATLIHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGSVGSEDQQLEPAHISPAIP-------VIITAVYSVVFVVGLVGNSLVMFV 83
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                                                                                                                                                                                                                                  KYRAA-----AFKLLLARKSRPRGFHRSRDTAGEVAG--DTGG 396
                                                                                                                                                                                                                                                                                                                              VVLAFIICWLPFHVGRIIYI--NTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWILASSVGISAIVLGGTKVR 202
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                                                                                                                                                                                                                                                                                                                                                                                    -----VFVFAFVIPVLIIIVCYTLMILRL-KSVRLLSG--SREKDRNLRRITKIVLV
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YNLISKKYRAAAFKLLLARKSRPRGFHRSR 384

YTVSSQQFRRVFVQVLCCRLSLQHANHEKR 373

180

LVN-VPSHRGLTCNRSSTRHHEQ----

121 124

61 66 20

RESULT 7 US-09-825-294-209

Sequence 209, Application US/09825294 Patent No. US20020004491A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun APPLICANT: Stolk, John A.

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124

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180 LVN-VPSHRGLTCNRSSTRHHEQ--

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Query Match Best Local ( Matches 111;

Local Similarity

Conservative

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US-09-966-871-76
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US-09-966-871-76
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                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 76, Application US/09966871 Patent No. US20020127539A1
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/966,871
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/236,302
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/288,644
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                            APPLICANT: Kopin, Alan S.

TITLE OF INVENTION: Assays for Identifying Receptors Having
TITLE OF INVENTION: Alterations in Signaling
                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 00398/512002
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PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 87
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                 ORGANISM: Homo sapiens
                                             TYPE: PRT
                                                                    LENGTH: 376
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US-10-039-645-76
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SEQ ID NO 76
LENGTH: 376
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APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Mar
                                                                                                                                                                                                                                                                                                                                   Matches 102;
                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/039,645
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/243,550
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 87
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TITLE OF INVENTION: and No. US20020147170Alfunctional Receptors as No. US2002014717
FILE REFERENCE: 00398/510002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
161 VLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPS 220
                                              117 MNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINI 176
                                                                                          101 SRPWVFGPLLCRLSLYVGEGCTYATLLHWTALSVERYLAICRPLRARVLVTRRRVRALIA 160
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                                                                                                                                      58 ITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQ-STVYL 116
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                                                                                                                                                                                  42 -TAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLFFDLYRLWR 100
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                   MESPFRGEPGPTCA---PSACLPPNSSAWFPGWAEPSNGSAGSEDAQLEPAHISPADPVE 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CIALGYTNSSLNPILYAFLDENFKRCFRDFCFPLKMRMERQSTSRVRNTVQDPA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYI--NTEDSRMMYFSQYFNI 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LFMKIC------VFIFAFVIPVLIIIVCYTLMILRL-KSVRL 254
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin
                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 336.5; DB : 24.6%; Pred. No. 5.2e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 336.5; DB 10; Length 24.6%; Pred. No. 5.2e-20;
                                                                                                                                                                                                                                                                                                                           76;
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                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                  ------CDERRCSPFPLGALVPV- 41
                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length
                                                                                                                                                                                                                                                                                                                              158; Indels
                                                                                                                                                                                                                                                                                                                                                                            376;
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RESULT 12
US-09-813-114-23
; Sequence 23, Application US/09823114
; Patent No. US20020061554A1
; GENERAL INFORMATION:

	-RDTA	34 PLGALVPVTAVCLCLEVVGVSGNVVTVMLIGRYKDMRTTINLYLGSMAVSULLILLGGLEF 93
LILARKSRPRGFHRS 383	Qy 331 YFSQYFNIVALQLFYLSASINPILYNLISKXYRAAAFKLLLARKSRPRGFHRS	Similarity 27.4%; Pred. No. 6.Le-20; Indels 67; Ga
VQVFVLVQGLGVQ 288	Db 236 IRRL-RGVRLLSGSREKDRNLRRITRLVLVVVAVEVGCWTEVQVFVLVQGLGVQ	09-823-114-23 uery Match 15.6%; Score 335.5; DB 10; Length 367;
AYFFLPFLCLSILYGLI 270	211 199	NAME/KEY: MODIFIED SILE LOCATION: group(19, 26, 37) LOCATION: group(19, 26, 37) OTHER INFORMATION: /note= "extracellular Asn residues OTHER CONSENSUS SILES FOR N-linked glycosylation" SEQUENCE DESCRIPTION: SEQ ID NO: 23:
	QY 151 TRRRVRALIAVLMAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLMSSPPLML	TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear FEATURE:
VERYLAICRPLRARVLV 150  :  :    :  VDRYVAICHPIRALDVR 159	Qy 94DLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLV 150	TELEX: 90-4030 MRSNFOERSWSH INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 367 amino acids
LGSMAVSDLLILLGLPF 93 : :: ::   :       IFNLALADTLVLLTLPF 103	Qy 34 PLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPF 93	REPERENCE/DOCKET NUMBER: 22000-20526.22 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500 TELEFAX: (202) 887-0763
Length 36/; Indels 73; Gaps 12;	Query Match 15.5%; Score 333.5; DB 9; Best Local Similarity 26.8%; Pred. No. 8.9e-20; Matches 100; Conservative 68; Mismatches 132;	
	Rattus norvegicus A-15	PRIOR APPLICATION DATA:  APPLICATION NUMBER: 09/148,351  ETITUR DATE: CINCRONED
		APPLICATION NUMBER: US/09/823,114 FILING DATE: 29-Mar-2001 CIASSIPICATION: <unknown></unknown>
	NUMBER OF SEQ ID NOS: 36 NUMBER OF SEQ ID NOS: 36 SOFTWARE: Patentin version 3.0	OPERATING SYSTEM: PC-DOS/MS-DOS  OPERATING SYSTEM: PC-DOS/MS-DOS  CURRENT APPLICATION DATA:
	; FILE REFERENCE: UM-06962; CURRENT FILING DATE: 2002-03-01	COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible
ACIDS	APPLICANT: OWYANG, Chung APPLICANT: OWYANG, Chung TITLE OF INVENTION: ORPHANIN FQ RECEPTOR NUCLEIC	COUNTRY: USA ZIF: 20006-1888 COMPRESS BEADALE BOOM.
		STREET: 2000 PENNSYLVANIA AVENUE, NW, SUITE 5500 CITY: WASHINGTON STATE: DC
	RESULT 13 US-10-087-345A-15	
	Db 347 RSIAKDVA 354	KEITH, DUANE E. TITLE OF INVENTION: OPIOID RECEPTOR GENES NIMBER OF SCOURNOES: 25
	Qy 384 RDTAGEVA 391	S
CCASALRRDVQVSDRV 346	Qy 331 YESQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPKGFHKS	19-823-114-23 19-823-114-23 quence 23, Application US/09823114  tent No. US20020061554A1
QVFVLAQGLGVQ 288	Db 236 IRRL-RGVRLLSGSREKDRNLRRITRLVLVVVAVFVGCWTFVQVFVLAQGLGVQ 288	111 -CIAĹGYTNSŚLNPIĹYAFLDENFKRCFRDFCFPLKMRMEF
FIVPVLVISVCYSLM 235	199	
-	CRPSPAQLGALRVMLWVT	
GISVVEGINGTARIASSELASSELAW 210 	QY 151 TRRRVRALIAVIMAVALLSAGPELELVGVEQDEGISVVEGLNGTALIASSHASSEFFUND	220LFMKICVFIFAFVIPVLIIIVCYTLMILRL-KSVRL 254 281 LRGDAASGRERGHROTKRVLLVVVLAFIICWLPFHVGRIIVINTEDSRWMYFSQYFNI 338
	Db 104 QGTDILLGPWPFCNALCKTVIAIDYYNMFTSTFTLTAMSV	221 GPETAEAAALFSRECRPSPAQLGALRVMLWYTTAYFFLPFLCLSILYGLIGRELWSSRRP 280
:     :       :     :   :   :   :   :	Qy 94DLYRLWRSRPWVFGPLLCRLSLYVGEGCTTATLLHWIALSVERILHALGREHAMANVEV	177 CIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWWD 219

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION MUNBER: US/09/823,114

FILING DATE: 29-Mar-2001

CLASSIFICATION UNDER: 09/148,351

FILING DATE: -UDKnown>

PRIOR APPLICATION NUMBER: 09/148,351

FILING DATE: -UDKnown>

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REGISTRATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEPAX: (012) 887-0763

TELEPEX: 90-4030 MESUFORMATION:

TELEPAX: (202) 887-0763

TELEPC SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 367-36165

밁 Ş US-09-823-114-23

Query Match Best Local 9

US-09-992-331-16

GENERAL INFORMATION:

APPLICANT: FEDER, APPLICANT: MINT

MINTIER,

JOHN N. GABE

APPLICANT: RAMANATHAN, CHANDRA S.
APPLICANT: HAWKEN, DONALD R.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY18,
TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
TITLE OF INVENTION: CELLS

FILE REFERENCE: D0048NP

Sequence 16, Application US/09992331 Publication No. US20030022186A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/992,331
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/208,540
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/261,782
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/248,483
PRIOR APPLICATION NUMBER: 60/248,483
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                               Sequence 16, Application US/09966782A Publication No. US20030022183A1 GENERAL INFORMATION:
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Best Local
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                                                            APPLICANT:
                                                                                                      APPLICANT: Battaglino, APPLICANT: Feder, J. 1
                    APPLICANT:
                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                            PLPEEPAFFGLYFLVVALP--YANSCANPILYGFLSYRFK-QGFRRILLRPSR 342
                                                                                                                                                                                                                                                                                                                                                                                                                     ELWSSRRPLR------GPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQNALSYWPFGSLMCRLVMAVDGINQFTSIFCLTVMSVDRYLAVVHPTRSARWRTAPVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĠILISLVYLVVĊ--VVĠLLGNSLVIYVVLRHTSSPSVTSVYILNLALADELFMLGLPF-L 101
                                                                                                                                                                                                                                                                                                                                                                               KVRSTTRRVRAPSCOWVOAPACORRRRSERRVTRMVVAVVALFVLCWMPFYLLNIVNVVC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPPSGPETAEAAALFSRECR----PSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMVSAAVWVASAVVVLPVVVFSGV-----
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                                                          Feder, J. N. Mintier, G. Ramanathan, C.
Westphal, R. Hawken, D. R. Cacace, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,731
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/268,580
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/315,423
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 64
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APPLICANT: KOYNACKEY, M. G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY7,
TITLE OF INVENTION: EXPRESSED HIGHLY IN SPINAL CORD
FILE REFERENCE: D0044NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
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288 NPÍVÝALVSKHFR-KGFRKICÁGLLRP----APRRASGRVS 323
                                         351 NPILYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVA 391
                                                                                                                                     298 RVLLVVVLAFIICWLPFHV-----GRIIYINTEDSRMMYFSQYFNIVALQLFYLSASI 350
                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                         179 VEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPS 238
                                                                                                                                                                                                                                                                                                                                                                             106 FLTMHASSFTLAAVSLDRYLAIRYPLHSRELRTPRNALAAIGLIWGLALLFSGPYLSYYR 165
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                                                                                                                                                                                                                                                                                      166 QSQLANLTV-----
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                                                                                                                                                                                                                              PAQLGALRVMLWVTTAY-FFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSQGAENTSQEGGSGGWQ------PEAVLVPL--FFALIFLVGTVGNALVLA 48
                                                                                        RMIIIVAVLFCLCWMPHHALILCVWFGRFPL----TRATY---ALRILSHLVSYANSCV 287
                                                                                                                                                                                 -----RAMDLCTFVFSYLLÞVLVLSLTYARTLRYLWRTVDÞV--TÁGSGSQRAKRKVT 235
                                                                                                                                                                                                                                                                                                                                                                                                                         EGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGRYRDMRTTTNLYLGSMAVSDL-LILLGLPFD--LYRLWRSRPWVFGPLLCRLSLYVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                 ----- 184
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16;

67;

Gaps

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Job time : 16 secs Search completed: March 16, 2003, 15:08:53

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     857
855
769.5
768.5
668.5
638.5
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                          Match
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2156
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               35.7
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            US-09-077-675A-13
US-09-077-675A-3
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US-08-818-876A-2
US-08-818-876A-4
US-09-472-880-2
US-08-818-876A-4
US-09-113-283-10
US-08-832-399-2
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US-08-831-283-10
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15.3	15.3	15.3	15.3	15.3	15.4	15.4	15.4	15.4	15.4	15.5	15.5	15.5	15.5	15.5	15.5	15.5	15.5	
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#### ALIGNMENTS

RESULT 1 US-09-077-675A-13

Sequence 13, Application US/09077675A Patent No. 6242199

GENERAL INFORMATION:

Pai, Lee-Yuh Feighner, Scott C Howard, Andrew D.

Scott C.

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-077-675A-13
 Query Match
Best Local Similarity
                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESSEG for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3 JUN-1998
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 1959
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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APPLICANT: Van Der Ploeg, Leonardu.
TITLE OF INVENTION: RECEPTOR ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O.
CITY: Rahway
STATE: NJ
                                                                                                    LENGTH: 366 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                       SS: single
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O. Box 2000, 126 E. Lincoln Ave.
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44.5%;
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PARTECT NO. 6242199
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                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardu:
TITLE OF INVENTION: RECEPTOR ASSAY
                                                                                                                                                                                                 ATTORNEY JAGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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P.O. Box 2000, 126 E. Lincoln Ave
353 amino acids
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardu
TITLE OF INVENTION: RECEPTOR ASSAY
                                    ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 RYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 WLPFHYGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAF 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 VFFFLPVFCLTVLYSLIGRKLW---RRKRGEAAVGSSLRDQNHKQTVKNLAVVVFAFILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 WPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNL 75
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                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 3-JUN
                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
   NAME: Cocuzzo, Anna L. REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rahway
                                                                                              FILING DATE:
                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDAPPENDSLVEELLPLPPTPLLAGVTATCVALFVVGIAGNLLTMLVVSRFREMRTTINL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLGSMAVSDILITLGTPFDLYRIMRSRPWVFGPLLCRISTYVGEGCTYATTLHMTALSVE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLSSMAFSDLLIFLCMPLDLFRLWQYRPWNLGNLLCKLFQFVSESCTYATVLTITALSVE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLPPHVGRYLFSKSLEPGSVEIAQISQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLIGFEPFSQRKLSTLKDESSR-----AWTESSIN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07065-0900
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                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                3-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee-Yuh
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                                                                                                                                                                                                                                              US/09/077,675A
            42,452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DPRD-----TNECRATEFAVRSGLLTVMVWVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leonardus H.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 857; DB 4;
Pred. No. 1.6e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09077675A
Patent No. 6242199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                           COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                  TITLE OF
                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                     STREET: E. STREET: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 ASINPILYNLISKKYRAAAFKLL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AAINPILYNIMSKKYRVAVFKLL 336
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                                                COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 YVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLF 175
   APPLICATION NUMBER:
                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NILTMLVVSRFRELRTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPWNFGDLLCKLFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 NVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLMRSRPWVFGPLLCRLSL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sil
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 WNAT--PSEEPEPNVTLDLDWDASPGNDSLPDELLPLFPAPLLAGVTATCVALFVVGISG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATEFAVRSGLLTVMVMVSSVFFFLPVFCLTVLYSLIGRKLM--RR--RGDAAVGASLRD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPS--PAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG---RE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNHKQTVKMLAVVVFAFILCWLFFHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVIMAVAFCSAGPIFV 179
                                                                                                                                                                                                                                                                                    INVENTION:
                                                                                                                                                                                                      E: Merck & Co., Inc.
P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                            Pong, Sheng-Shung
Van Der Ploeg, Leonardus H.T.
VENTION: RECEPTOR ASSAY
                                                                                                                                                                                                                                                                                                                                    Pai, Lee-Yuh
Feighner, Scott C
Howard, Andrew D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732-594-4720
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                                                                         IBM Compatible
                                                                                               Diskette
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48.0%; Pred. No. 2.2e-65;
ative 52; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                        Scott C.
US/09/077,675A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TNEC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 364;
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                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09077675A Patent No. 6242199
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pai, Lee-Yuh
APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Howard, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                               CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 FHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                334 GFEPFSORKLSTLKDESSR-----AWTESSIN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 LARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 AYFFLPFLCLSILYGLIGRELMSSRRPLRGPAASGRERGHRQTKRVLLVVVIAFIICWLP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 -----DP--W-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 RIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPS--PAQLGALRVMLWVTT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 IFFFLPVFCLTVLYSLIGRKLWRRRRGDAVVGASLRDQNHKQTVKMLAVVVFAFILCWLP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 RYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVLVGVEHE-----NGT- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 RYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTA 195
                                      CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 39.6%; Score 854; DB 4; Length 361; Local Similarity 45.8%; Pred. No. 2.9e-65;
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 YLSSMAFSDLLIFLCMÞLDLVRÍMQYRÞMNFGDLLCKLFQFVSESCTYATVLTITALSVE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 WDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAGNLLIMLVVSRFRELRTTINL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 WPALPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 42
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 3-JUN-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182; Conservative
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USA
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ZIP: 07065-0900 COMPUTER READABLE FORM:

MEDIUM TYPE: Disactible Compatible

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                                                                                                                                                                                    Sequence 7, Application US/09077675A Patent No. 6242199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
            APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardu
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1:
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                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 FAVRSGLLTVMVMVSSVFFFLÞVFCLTVLÝSLÍGRKLM---RRKRGEAAVGSSLRDQNHK 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 3-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLVVSRFREMRTTTNLYLSSMAFSDLLIFLCMFLDLFRLWQYRFWNLGNLLCKLFQFVSE 60
                                                                                                                                                                                                                                                                                                                                        PILYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
                                                                                                                                                                                                                                                                                                                                                                                <u>ÓTVKMLAVVVFAFILCWLÞFHVGRYLFSKSLEPGSVEIAQISQYCNLVSFVLFYLSAAIN</u>
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                                                  RMATION.

Pai, Lee-Yuh

Feighner, Scott C.

Howard, Andrew D.

Pong, Sheng-Shung

Pong, Sheng-Shung

Remardus H.T.
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Merck & Co.; Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.7%; Score 769.5; DB 4;
46.3%; Pred. No. 3.8e-58;
40. Mismatches 80;
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                                                                                                                                                              RESULT
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                                                                                                         ; Sequence 12, Application US/09077675A
; Patent No. 6242199
                                                                                                                                               US-09-077-675A-12
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                                                   GENERAL INFORMATION:
APPLICANT: Pai, Le
APPLICANT: Feighne
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                   APPLICANT:
 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                    355 YNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                              EHE----NGT-----DP--W-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 35.6%; Score 768.5; DB 4
Similarity 46.2%; Pred. No. 4.7e-58;
63; Conservative 51; Mismatches 82
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Pai, Lee-Yuh
reighner, Scott C.
Howard, Andrew D.
Pong, Sheng-Shung
Van Der Ploeg, Leonardus H.T.
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US-09-077-675A-10
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                   Sequence 10, Application US/09077675A Patent No. 6242199
GENERAL INFORMATION:
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     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLL.
STATE: N.
COUNTRY: USA
TTP: 07065-0900
TTP: TRADABLE F
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                         386 TAGEVAGDTGGDTVGYTETSAN 407
                                                                                                                                                                                                                                                                                                                                       269 LIGRELWSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDS- 327
                                                                                                                                                   259 ESSR-----AWTESSIN 270
                                                                                                                                                                                                                         199 SLEIAQISQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPFSQRKLSTLKD 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 LPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLV 150
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TELEFAX: 732-594-4720
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. CITY: Rahway
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                                                                                                                                                                                                                                                   --RMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRSRD 385
                                                                                                                                                                                                                                                                                                                                                                           -------DINECRPTEFAVRSGLLTVMVWVSSIFFFLPVFCLTVLYS 138
                                                                                                                                                                                                                                                                                                                                                                                                               SRAPPPSPPSGPETAEAAALFSRECRPS--PAQLGALRYMLWYTTAYFFLPFLCLSILYG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKGRVKLVIFVIWAVAFCSAGPIFVLVGVEHE-----NGT------DP--W- 98
                                                                                                                                                                                                                                                                                                   LIGRKLWRRRRGDAVVGASLRDQNHKQTVKMLAVVVFAFILCWLPFHVGRYLFSKSFEPG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRRRVRALIAVLWAVALLSAGPFLFLYGYEQDPGISVVPGLNGTARIASSPLASSPPLWL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPLDLVRLWQYRPWNFGDLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 amino acids
Pai, Lee-Yuh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%; Score 668.5; DB 4; Length 271; 44.7%; Pred. No. 1.4e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR ASSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Mismatches
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RESULT 9 US-09-077-675A-5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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   260
                                      295
                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                           200
                                                                                                                                                 182
                                                                                                                                                                                                                   122 VSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   117 VGBGCTYATILHMTALSVERYLAICRELRARVLVTRRRVRALIAVLWAVALLSAGPELFL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                           62 LLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPWNFGDLLCKLFQF 121
                                                                                                                                                                                                                                                                                                                           57 VVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COCUZZO, Anna L. REGISTRATION NUMBER: 42, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 3-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                   2 WNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAGN 61
                                                                                                                                                                                                                                                                                                                                                                                                    5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
QTVKMLGGSQRALRLSLAGPILSLCLLP 287
                                                                                           PS--PAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHR 294
                                   QTKRVL-----LVVVLA---FIICWLP 313
                                                                    PTEFAVRSGLLTVMVWVSSIFFFLPVFCLTVLYSLIGRKLWRRRRGDAVVGASLRDQNHK 259
                                                                                                                                                                               VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSSPPSGPETAEAAALFSRECR 236
                                                                                                                                               VGVEHE------NGT-----DP--W-
                                                                                                                                                                                                                                                                                                                                                                                                                                           143; Conservative
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P.O. Box 2000, 126 E. Lincoln Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.6%; Score 638.5; DB 4; 43.6%; Pred. No. 5.4e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 627; DB 4; Length 289; Best Local Similarity 44.3%; Pred. No. 5.1e-46; Matches 137; Conservative 43: Micmatches
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APPLICANT: Pai, La
APPLICANT: Feighn
APPLICANT: Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pai, Lee-Yuh
APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASTSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
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COMPUTER READABLE FORM:
TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          122
                                                                                                                                                                                                  177
  257 NHKQTVKML 265
                                       292 GHROTKRVL 300
                                                                          200 ATEFAVRSGLLTVMVWVSSVFFFLPVFCLTVLYSLIGRKLW---RRKRGEAAVGSSLRDQ
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                     57 VVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
                                                                                                                                                                                                                                                                       VGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFL 176
                                                                                                                                                                                                                                                                                                                  LLTMLVVSRFREMRTTTNLYLSSMAFSELLIFICMPLELFRIMQYRPWNLGNLLCKLFQF 121
                                                                                                                                                                                                                                        VSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVIWAVAFCSAGPIFVL 181
                                                                                                                                                                                                                                                                                                                                                                                               WNATPSEEPGPNLTLPDLGWDAPPENDSLVEELLPLFPTPLLAGVTATCVALFVVGIAGN 61
                                                                                               PS--PAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG---RER 291
                                                                                                                                                           VGVEHD-----NGT----
                                                                                                                                                                                                VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSSPPSGPETAEAAALFSRECR 236
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P.O. Box 2000, 126 E. Lincoln Ave
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linear
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LENGTH: 415;
TYPE: PRT;
ORGANISM: HOMO SAPIENS
US-09-545-944-2
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                                                                                                                          Sequence 45, Application US/08118270; Patent No. 5508384; GENERAL INFORMATION:
                                                                                                                                                                                    US-08-118-270-45
                                                                                                                                                                                                        RESULT 11
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Patent No. 6461836
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 5
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CURRENT APPLICATION NUMBER: US/09/545,944
CURRENT FILING DATE: 2000-04-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: AMES, APPLICANT: ELSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
             APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
                                                                                                                                                                                                                                                                                                                                                                                                          235 LYYLMALRIKKDKSLEADEGNANIQRPCR------KSVNKMLFVLVLVFAICWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                           266 LYGLIGRELWSSR------RPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 PLWLSRAPPPSSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 LYTRRYVRALIAVLWAVALLSAGPFLFLVGVE--QDPGISVVPGLNGTARIASSPLASSP 206
                                                                                                                                                                                                                                                                                                                                                                         314
                                                                                                                                                                                                                                                              343 S----SFHK 347
                                                                                                                                                                                                                                                                                                 372 ARKSRPRGFHR 382
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ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSTRRALRILGIVMGFSVLFSLPNTSIHGIKFHYFPNGSLVPG------SATCTVIK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGLPFDLYRLWRSRPWVFGPLLCKLSLYVGEGCTYATLLHWTALSVERYLAICRPLRARV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL 96
                                                                                                                                                                                                                                                                                                                                  LGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMWI-----YNFIIQVISFLFYLLPMTVISV 234
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RESULT 12
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                                                                         Sequence 45, Application PC/TUS9308528 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
TELEX: 248423
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILLING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                         311 LACLFCPGWPLIRRKKRP 328
                                                                                                                                                                                                                                                                                                                           312 LPFHVGRIIYINTEDSRMMYFS--QYFNIVALQLFYLSASINPILYNLISKKYRAAAFKL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                  275 WSSRRPLRGPAASGR---------ERGHRQTKR----VLLVVVLAFIICW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 PSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFL-PFLCLSILYGLIGREL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 KKFISAIWLASALLAIPMLFTLGLONRSGDGTHPG-----GLVCTPIVDT------ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 RALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 YNFIWHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHPFKAKTLMSRSRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 YRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHWTALSVERYLAICRPLRARVLVTRRRV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 VPVTAVCLCLFVVGVSGNVVTVMLIGR----YRDMRTTTNLYLGSMAVSDLLILLGLPFDL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Townsend, Kevin REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VLVTÄIYLALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLSSLÄLSDLLILLMV--EL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CENGTH:
                                                                                                                                                                                                                                                                                   ĹPY----LCYISDEQWRTFLEDFYHYFYMLTNALFYVSSAINFILYNLVSANFRQVFLST 310
                                                                                                                                                                                                                                                                                                                                                                          TVM----VHQAAEQGRVCTVGTHNGLEHSTFNMRIEPGRVQALRHGVLVLRAVVIAFVVCW 254
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.5%; Score 463; DB 1; Length 35: 32.3%; Pred. No. 6.2e-32; tive 55; Mismatches 111; Indels
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RESULT 13
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Best Local Similarity
Matches 122; Conserv
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TELEX: 248633
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Townsend, Kevin G.
REGISTAE 34,033
REFERENCE/DOCKET NUMBER: MUJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: BROWDY AND NEIMARK
                                                                              311 LACLFCPGWPLIRRKKRP 328
                                                                                                                                                                              312 LPFHVGRIIYINTEDSRMMYFS--QYFNIVALQLFYLSASINPILYNLISKKYRAAAFKL 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 VPVTAVCLCLFVVGVSGNVVTVMLIGR---YRDMRTTTNLYLGSMAVSDLLILLGLPFDL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YNFIWHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHPFKAKTLMSRSRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US93/08528 FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VLVTAIYLALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLSSLALSDLLILLWV--EL 59
                                                                                                                                               LPY----LCYISDEQWRTFLFDFYHYFYMLTNALFYVSSAINFILYNLVSANFRQVFLST 310
                                                                                                                                                                                                                                                                       WSSRRPIRGPAASGR--------ERGHROTKR----VLLVVVLAFIICW 311
                                                                                                                                                                                                                                                                                                                                                                                        KKFİSAIWLASALLAIPMLTTLGLQNRSGDGTHPG-----GLVCTPIVDT------ 164
                                                                                                                   TVM----VHQAAEQGRVCTVGTHNGLEHSTFNMRIEPGRVQALRHGVLVLRAVVIAFVVCW 254
                                                                                                                                                                                                                                                                                                              -----ATVKVVIQVNTFMSFLFPMLVISILNTVIANKL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.5%; Score 463; DB 5; Length 353; nilarity 32.3%; Pred. No. 6.2e-32; Conservative 55; Mismatches 111; Indels
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Sequence 2, Application US/08858876A Patent No. 6022856

APPLICANT:

STATE:

STREET:

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GENERAL INFORMATION:
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FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Jacobson, Price, Holman & Stern, PLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Type 2 Neurotensin Receptor TITLE OF INVENTION: (hNT-R2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                         272 RELWSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDSR---
                                                    331 PLYNFYHYFYMVTNTLFYVSSAVTPLLYNAVSSSFR----KLFLEAVSSLCGEH 380
                                                                                                                                                                                                                                                                                  212 RAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIG 271
                                                                                                                                                                                                                                                                                                                                  181 ETADGEPEPASRVCTVL--VSRTALQVFIQVNVLVSFVLFLALTAFLNGVTVSHLLALCS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 ATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGV---- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 PPWPALPP---CDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLI-----GR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 LRH-----HVLSLALAGLILLLLVGVÞVELYSFVWFHYÞWVFGDLGCRGYYFVHELCAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                         ATVLSVAGLSAERCLAVCOPLRARSILTPRRTRWLVALSWAASIGLALPMAVIMGQKHEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRDMRTTTNLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPRPSSNPGLSLDARLGVDTRLWAKVLFTALYALIWALGAAGNALSVHVVLKARAGRAGR 67
                                                                                             -MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFH 381
                                                                                                                                                                                                                                           QVPSTSTP-GSSTPSRLELLSEE-----GLLSFIVWKKT---
                                                                                                                                                                                                                                                                                                                                                                             -----EQDPGISVVPGLNGTARIASS------PLASSPPL-----WLS
                                                                                                                                                QVSLVRHKDVR-----RIRSLQRSVQVLRAIVVMYVICWLPYHARRLMYCYVPDDAWTD
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Patent No. 6274333
GENERAL INFORMATION:
APPLICANT: Daniel CAPUT
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Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          212 RAPPPSPPSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLSILYGLIG 271
                                                                                                                                                                                                                                                                           181 ETADGEPEPASRVCTVL--VSRTALQVFIQVNVLVSFVLPLALTAFLNGVTVSHLLALCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 YRDMRTTTNLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWYFGPLLCRLSLYYGEGCTY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PPRPSSNPGLSLDARLGVDTRIWAKVLFTALYALIWALGAAGNALSVHVVLKARAGRAGR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price,
STREET: 400 Seventh Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,880
FILING DATE: 28-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER READABLE FORM:
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PLYNEYHYFYMVTNTLFYVSSAVTPLLYNAVSSSFR----KLFLEAVSSLCGEH 380
                                        -MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFH 381
                                                                                                                               RELWSSRRPLRGPAASGRERGHRQTKRYLLVVVLAFIICWLPFHVGRIIYINTEDSR---
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                                                                                                                                                                                                                                                                                                                                                                                                          ATLLHMTALSVERYLAICRPLRARVLYTRRRVRALIAVLWAVALLSAGPFLFLVGV---- 179
                                                                                         QVSLVRHKDVR-----RIRSLQRSVQVLRAIVVMYVICWLPYHARRLMYCYVPDDAWTD
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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Pascual FERRARA
Vita NATALIO
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31.2%; Pred. No. 4.4e-27;
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Length 410;

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TOPOLOGY:

LENGTH:

Query Match Best Local 9 Matches 129;

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Sequence 4, Appli Patent No. 602285

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acids
TYPE: amino acid
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APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
339 VALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGD 393
                                                                  282 RHKDASQIRSLQHSAQVLRAIVAVYVICWLPYHARRLMYCYIPDDGWTNELYDFYHYFYM 341
                                                                                                                                                           235 ALYS-QVPSASAQVSSTPSRLELLSE------EGLLGFITWRKTLSLGVQASLV 281
                                                                                                                                                                                                          229 ALFSRECRPSPAOLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASG 288
                                                                                                                                                                                                                                                      186 EPEPASRVCTVLVSRATLQVFIQVNVLVSFALPLALTAFL------NGITVNHLM 234
                                                                                                                                                                                                                                                                                                   180 EQDPGISVVPGLNGTARIA------SSPLASSPPLWLSRAPPPSPPSGPETAEAA 228
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APPLICANT: Pascale CHALON
APPLICANT: Pascual FERRARA
APPLICANT: Vita NATALIO
TITLE OF INVENTION: Type 2 Neurotensin Receptor
TITLE OF INVENTION: (hNT-R2)
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GRLRYHVLSLALSALLLLLLVSMPMELYNFVWSHYPWVFGDLGCRGYYFVRELCAYATVLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 -TINLYLGSMAVSDLLILL-GLPFDLYR-LWRSRPWVFGPLLCRLSLYVGEGCTYATLLH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 PWPALP-----PCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRT 71
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FILING DATE: 19-SEP-1997
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                                                                                                       RERGHROTK-----RVLLVVVLAFIICWLEFHVGRIIYINTED----SRWMYFSQYFNI 338
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

10	οω	7 0	ហ	4.	ω	N	1	Result No.
901	1575	1575	2149	2149	2149	2149	2156	Score
41.8	73.1	73.1	99.7	99.7	99.7	99.7	100.0	Query Match
363	386	386	501	412	412	412	412	Query Match Length DB
21	2 2	21	22	22	22	21	21	DB B
AAY54147	AAB62653	AAB68477 AAY54146	AAG65822	AAB68478	AAB62652	AAY54145	AAB02854	ID
Amino acid sequenc The puffer fish mo	Short form of moti	Amino acid sequenc Amino acid sequenc	Human GPR38 varian	Amiño acid sequenc	Long form of motil	Amino acid sequenc	Human G protein co	Description

45	44	43	42	41	40	39	38	37	36	35	34	IJ IJ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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#### ALIGNMENTS

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99US-0123944. 99US-0123945. 99US-0123946. 99US-0123946. 99US-0123948.	98US-0110416. 99US-0120416. 00HG-011061	98US-0109213.	98US-0170496. 98US-0108029.	99WO-11824.055		2.					screening; therapeutic; pharma	ein coupled receptor; GPCR; transmembrane receptor;		protein coupled receptor hGPR38 (V297K) protein SEO ID NO:130	(first entry)				standard; Protein; 412 AA.	

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28-MAY-1999;
28-MAY-1999;
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28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents
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29-SEP-1999;
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                KYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG
                                                                    LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK
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KYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG
                                                                                                            QLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVL
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                                                                                                                                                                                                QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPA
                                                       LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK
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                                                                                                                                                                                                                                                                                                                      The present sequence represents splice variant MTL-RIA of the motilin creceptor. The gene encodes a G-protein coupled receptor, and is CC designated MTL-RI (also GPR38). Two spliced forms of GPR38 exist, CC MTL-RIA (see AAV54145) and MTL-RIB (see AAY54146). MTL-RIA is a CC functional seven transmembrane domain form, and MTL-RIB is a truncated five transmembrane domain. The MTL-RI proteins are used to identify CC agonists and antagonists which can be used for treating gastric motility CC disorders, functional defects, disorders secondary to neurological CC disorders e.g. scleroderma, paraneoplastic syndromes radiation induced CC dysmotility, diabetes, infections, stress related motility disorders, psychgenic disorders, gastroparesis, gastro-oesophageal reflux disease, CC psychgenic disorders, idiopathis pseudo obstruction, acute faecal constipation, chronic idiopathis pseudo obstruction, acute faecal constipation, conscuperative ileus, gallstones, infantile collic, irritable bowel syndrome, non-ulcer dyspepsion, non-cardiac chest pain and CC diarrhoea. They can also be used in the preparation for colonoscopy, cendoscopy and incharation in the preparation for colonoscopy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel receptor protein for screening compounds used in irritable bowel syndrome, constipation and other gastri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9964436-A1
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The invention relates to a method of forming a reversible peptide receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB62649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pancreatic enzymes and hormones, secretion of insulin-like growth factor 1, secretion of non-zsig33 proteins. It is useful for modulating growth hormone secretion in a mammal having a disease associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forming reversible peptide receptor complex for purifying cell a peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptid
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insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
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                                                                                   29-OCT-1999;
                                                                                                                                                                                                             10-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB68478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB68478 standard; Protein;
                                                                                                                                             25-OCT-2000; 2000WO-US29426.
                                                                                                                                                                                                                                                                          WO200132710-A1
                                                                                                                                                                                                                                                                                                                                                                                                 gastroparesis;
                                                                                                                                                                                                                                                                                                                                                                                                                       Motilin receptor; gastrointestinal disease; gastric motility disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-2001
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                                                                                      99US-0162264.
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Pred. No. 2.2e-194;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor amino acid sequence, useful for identifying compounds for treating diarrhoea in humans
                  GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic; anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic; antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant; antiulcer; antiemetic; cardiant; vaccine; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human GPR38V polypeptide and polynucleotide, useful for treating e.g. bacterial, fungal, protozoal and viral infections, cancers or allergies, as vaccines, and for identifying agonists and antagonists potentially useful in therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane bound or soluble receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elshourbagy N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                           MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPPLGALVPVTAVCLCLFVVGVSGNVVTV 149
                                                                                                                                                                                                                                                                                                                                                                                              MLIGRYRDMRTTTNLYLGSMAVSDLLI
                                                                                                                                                                                                                                                                                                                                     MLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
                                                                                                                                                                                                                                                                      LVVVLAFIICWLPFHYGRIIYINTEDSRMMYFGQYFNIVALQLFYLSASINPILYNLISK
                                                                                                                      QLGALRVMLWVTTAYFFLFFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTVRVL
                                                                                                                                             QLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVL
                                                                                                                                                                                     QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPA
                                                                                                                                                                                                                                                    CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE
                KYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG
                                                           LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK
                                                                                                                                                                                                                      QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPA
KYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                             411;
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Pred. No. 2.8e-194;
0; Mismatches 1;
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Best Local Similarity
Matches 343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a rabbit motilin receptor polypeptide. The specification describes an unique sequence present in exon 1 of the dog motilin receptor, which is not present in human or Sphaeroides nephelus 7587 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect motilin receptor activity. Motilin receptor polynucleotides and polypeptides are used to identify therapeutic compounds which are useful for treating gastrointestinal diseases and disorders such as gastric motility disorders, gastroparesis, irritable bowel syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 18; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor amino acid sequence, useful for identifying compounds for treating diarrhoea in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF85448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Motilin receptor; gastrointestinal disease; gastric motility disorder; gastroparesis; irritable bowel syndrome; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2000; 2000WO-US29426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a rabbit motilin receptor polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                diarrhoea.
                                                                                                                                                    CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVB 180
                                                                                                                                                                                                                  MLIGRYRDMRTTINLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
                                                                                                                                                                                                                                                                                  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTV 60
QLGLLRVMLWVTTAYFFLPFLCLSILYGLIARQLWRGRGPLRGPAATGRERGHRQTVRVL
                             QLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVL 300
                                                                                             QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPSPA
                                                               QDPAVFAAPDRNGTV-----PLDPSSP-----APASPPSGP-GAEAAALFSRECRPSRA
                                                                                                                              CTYASLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAALWAVALLSAGPFFFLVGVE
                                                                                                                                                                                           LLIGRYRDMRTTINLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGQLLCRLSLYVGEG 120
                                                                                                                                                                                                                                                            MGSPWNGSDGPEDAREPPWAALPPCDERRCSPFPLGTLVPVTAVCLGLFAVGVSGNVVTV 60
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                                                                                                                                                                                                                                                                                                                                         80.8%; Score 1741; DB 22; 83.7%; Pred. No. 7.1e-156;
                                                                                                                                                                                                                                                                                                                             Mismatches
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                                             disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychgenic disorders, gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathis pseudo obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile collic, irritable bowel syndrome, non-uncer dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy,
                                                                                                                                                                        The present sequence represents splice variant MTL-R1B of the motilin receptor. The gene encodes a G-protein coupled receptor, and is designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven transmembrane domain form, and MTL-R1B is a truncated five transmembrane domain. The MTL-R1D proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological
                                                                                                                                                                                                                                                                                                                                                                                     Novel receptor protein for screening compounds used in treating irritable bowel syndrome, constipation and other gastric condit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38; spliced form; MTL-R1A; MTL-R1B; gastric motility disorder; functional defect; neurological disorder; scleroderma; colonoscopy; paraneoplastic syndrome; radiation induced dysmotility; diabetes; infection; stress-related motility disorder; psychgenic disorder;
                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 5; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ45404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastroparesis; gastro-oesophageal reflux disease; constipation; chronic idiopathis pseudo obstruction; acute faecal impaction; postoperative ileus; gallstones; infantile collic; diarrhoea; irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac chest pain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith RG;
                                   and duodenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             duodenal intubation.
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                                 intubation.
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Sequence

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Score 1575;

DB

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Length 386;

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-I; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R; G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform
The invention relates to a method of forming a reversible peptide-
receptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsig33 peptide (comprising residues 24-37
of AAB62649), where the receptor binds to the zsig33 peptide. The method
is useful for purifying cells, purifying a peptide, stimulating signal
transduction in a cell expressing a receptor. It is also useful for
modulating secretion of hormones, neural development and/or utilization,
gastric contractility, nutrient uptake, secretion of digestive and
pancreatic enzymes and hormones, secretion of insulin-like growth factor
-I, secretion of non-zsig33 proteins. It is useful for modulating growth
                                                                                                                                                                                                                                                                                                                                                                                                          Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 106-109; 111pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormone secretion in a mammal having a disease associated with abnormal levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling,
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                                                                                                            MERCK & CO
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                                                                                                                                                                                                                                                                                         gastrointestinal disease; gastric motility disorder;
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99.7%;
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Pred. No. 3.2e-140;
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Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin r

receptor

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                             Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38; spliced form; MTL-R1A; MTL-R1B; gastric motility disorder; functional defect; neurological disorder; scleroderma; colonoscopy; paraneoplastic syndrome; radiation induced dysmotility; diabetes; infection; stress-related motility disorder; psychgenic disorder; gastroparesis; gastro-oesophageal reflux disease; constipation; chronic idiopathis pseudo obstruction; acute faecal impaction; postoparative ileus; gallstones; infantile collic; diarrhoea;
       12-JUN-1998;
                                                                      08-JUN-1999;
                                                                                                                                                                                                                                                                         Spheroides nephelus
                                                                                                                                                                                                                                                                                                                                                                 postoperative ileus; gallstones; infantile collic; diarrhoes irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             motilin receptor activity. Motilin receptor polynucleotides and polypeptides are used to identify therapeutic compounds which are useful for treating gastrointestinal diseases and disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The puffer fish motilin receptor protein encoded by clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes an unique sequence present in exon 1 of the motilin receptor, which is not present in human or Sphaeroides nephelus 7567 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY54147 standard; Protein; 363 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid sequence, useful for identifying compounds for treating diarrhoea in humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is encoded by exon 1 of a dog motilin receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLIGRYRDMRTTTNLYYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGBG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLGALRVMLWVTTAYFFLPFLCLCVLYGRIGRELRRRGPLRGRAASGRERGHRQAVRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230;
                                                                                                                                                                                                                                                                                                                                            duodenal intubation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
   8606800-SD86
                                                                   99WO-US12773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
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RESULT 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane domain form, and MTL-RLB is a truncated five transmembrane domain. The MTL-RLB proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychgenic disorders, gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathis pseudo obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile collic, irritable
23-JUL-2001 (first entry)
                                                                           AAB68479 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a motilin receptor (clone 75E7) which is related to the human motilin receptor of the invetion. The specification describes a G-protein coupled receptor, designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A (see AAY54145) and MTL-R1B (see AAY54145) and MTL-R1B (see AAY54146).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bowel syndrome, non-ulcer dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel receptor protein for screening compounds used in treating irritable bowel syndrome, constipation and other gastric conditions
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                                                                                                                                                                     290 TAMLSQNFNWASMVLCYLSASINPVVYNLMSRKYRAAAKRLFILHQ-RPKPAHRGQ 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLG 90
                                                                                                                                                                                                                                                   SIGCKLWKSKNDLQGPCALARERSHRQTVKILVVVVLAFIICWLPYHIGRNLFAQVDDYD
                                                                                                                                                                                                                                                                                        LIGRELMSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDSR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLV 150
                                                                                                                                                                                                            MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRSR 384
                                                                                                                                                                                                                                                                                                                                   ----HPDYNTG-----
                                                                                                                                                                                                                                                                                                                                                                   SRAPPPSPPSGPETAEAAALFSRECRPSPAQL--GALRVMLWVTTAYFFLPFLCLSILYG
                                                                                                                                                                                                                                                                                                                                                                                                        TRRRVQYIILALWCFALVSAAPTLFLVGVEYD-----NET--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPFDLYRLWKYVPWLFGEAVCRLYHYIFEGCTSATILHITALSIERYLAISFPLRSKVMV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLFPASTLIPVTVICILIFVVGVTGNTMTILIIQYFKDMKTTTNLYLSSMAVSDLVIFLC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                           Protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.8%; Score 901; DB 21; 50.3%; Pred. No. 1.3e-76; tive 56; Mismatches 77
                                                                                                                                                                                                                                                                                                                              ----QCKHTGYAISSGQLHIMIWVSTTYFFCPMLCLLFLYG
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Amino acid sequence of a motilin receptor polypeptide

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RESULT 12
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Motilin receptor; gastrointestinal disease; gastric motility disorder; gastroparesis; irritable bowel syndrome; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a bacterial motilin receptor polypeptide. The specification describes an unique sequence present in exon 1 of the dog motilin receptor, which is not present in human or Sphaeroides nephelus 75E7 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect motilin receptor activity. Motilin receptor polynucleotides and polypeptides are used to identify therapeutic compounds which are useful for treating gastrointestinal diseases and disorders such as useful for treating gastrointestinal diseases and disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sphaeroides nephelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric motility disorders, gastroparesis, irritable bowel syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 33-34; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, comprising unique regions from dog and motiful recept
amino acid sequence, useful for identifying compounds for treating
diarrhoea in humans .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor
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               AAY90666 standard;
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                                                                                                                                                                                                                                                                                                                                                                                     91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       μ
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                                                                                                                                                                                                                                                         SRAPPPSPPSGPETAEAAALFSRECRPSPAQL--GALRVMLWVTTAYFFLPFLCLSILYG 268
                                                                                                                                                                                                                                                                                       LPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLV 150
                                                                                            TAMLSQNFNWASMVLCYLSASINPVVYNLMSRKYRAAAKRLFLLHQ-RPKPAHRGQ 344
                                                                                                                                                          SIGCKLWKSKNDLQGPCALARERSHRQTVKILVVVVLAFIICWLPYHIGRNLFAQVDDYD
                                                                                                                                                                               LIGRELWSSRRPLRGPAASGRERGHRQTKRVLLVVVLAFIICWLPFHVGRIIYINTEDSR 328
                                                                                                                                                                                                                                                                                                                    TRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWL 210
                                                                                                                                                                                                                                                                                                                                                                                                                       SLFPASTLIPVTVICILIFVVGVTGNTMTILIIQYFKDMKTTTNLYLSSMAVSDLVIFLC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPEPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLG 90
                                                                                                                            MMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAFKLLLARKSRPRGFHRSR 384
                                                                                                                                                                                                                                                                                                                                                       AAF85450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKee K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US29426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0162264
                  Protein; 366 AA
                                                                                                                                                                                                                            ------QCKHTGYAISSGQLHIMIWVSTTYFFCPMLCLLFLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 901; DB 22;
Pred. No. 1.3e-76;
6; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                              185
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 CC and AAA30775-A30779). The mutant proteins of the invention contain a cc mutation in a portion of the protein comprising intracellular loop 3 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, CC (IC3) and is preferably Lys, when the endogenous residue at this cc position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Proceeding and the proteins are also useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research cc intentings for elucidating the roles of the receptors in normal and cc diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used conditions. Sequences AAY90643- AAY90677 and AAY90687 the mutant CC thuman GPCRs of the invention.
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                                                                                                                                        Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agonist; antagonist; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human mutant G protein-coupled receptor GHSR (V262K)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY90666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-329165/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Behan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2000
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                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 267-268; 341pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors, useful for identifying agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                             human GPCRs of the
 62
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                                                                    N
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                                VVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
                                                                 WNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAGN
                                                                                                   WNGSDGPEGA----REPPWPALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN
LLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFICMPLDLVRLWQYRPWNFGDLLCKLFQF 121
                                                                                                                                                           Similarity
                                                                                                                                                                                                            366 AA;
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                             invention.
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                                                                                                                                                          40.1%; Score 864.5; DB 2
44.7%; Pred. No. 3.7e-73;
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                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CW;
                                                                                                                                           Mismatches 106;
                                                                                                                                                                            DB 21;
                                                                                                                                               Indels
                                                                                                                                                                            Length 366;
                                                                                                                                               65;
                                                                                                                                               Gaps
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117 VGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFL

61 56

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RESULT 13
AAY69293
ID AAY69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
     Matches
                               Query Match
                                                                                      The present sequence represents a canine growth hormone secretagogue receptor (GHSR). The GHSR cDNA sequence was isolated from a canine cDNA library constructed from spleen. The GHSR polynucleotide is a source of probes and primers, which can be used to isolate GHSR genes from other species. It is also used for recombinant expression of the polypeptide. The GHSR polypeptide is used in assays to identify agonists, antagonist and inhibitors. Such identified compounds can serve as leads for the development of veterinary pharmaceuticals that can be used to treat dogs having illnesses in which inappropriate activity of the canine GHSR proteins involved. The polypeptides may also be used to raise antibodies for diagnostic and the processing involved.
                                                        Sequence
                                                                                  therapeutic purposes.
                                                                                                                                                                                                                                                              Claim 6; Fig 2; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A canine growth hormone secretagogue receptor (GHSR) protein.
                                                                                                                                                                                                                                                                                           agonists and antagonists
                                                                                                                                                                                                                                                                                                      A novel canine growth hormone secretagogue
                                                                                                                                                                                                                                                                                                                                                                            Howard AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine; growth hormone secretagogue receptor; GHSR; dog.
                                                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY69293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY69293 standard; Protein; 349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
               Local Similarity
    186;
                                                                                                                                                                                                                                                                                                                                                  2000-224272/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILYNIMSKKYRVAVFRLLGFEPFSQRKLSTLKDESSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTKKMLAVVVFAFİLCWLPFHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLSAAİN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTKRVLLVVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLSASIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTEFAVRSGLLTVMVWVSSIFFFLPVFCLTVLYSLIGRKLWRRRRGDAVVGASLRDQNHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS--PAQLGALRVMLWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSSPPSGPETAEAAALFSRECR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGVEHE-----NGT-----DP--W-----
                                                                                                                                                                                                                                                                                                                                      AAZ61492
                                                         349 AA;
  39.9%;
ilarity 46.2%;
Conservative 5
                                                                                                                                                                                                                                                                                                                                                                          Palyha OC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0095960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US17915
                                                                                                                                                                                                                                                                                                                                                                            Smith
  50;
           Score 859.5; DB Pred. No. 1e-72;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Tan CP;
                           DB 21;
                                                                                                                                                                                                                                                                                                     receptor used to identify
 98;
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 Indels
                          Length
                           349;
69;
Gaps
                                                                                                          The
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                                                                                                                                    Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                 Example 1; Page 167-169; 341pp; English.
                                                                                                                           agents
                                                                                                                                                                                                                      Behan DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; constitutively active;
                                                                                                                                                                                                                                                                          13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY90632 standard; Protein;
                                                                                                                                                                                                                                                                                                                             20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                        agonist; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90632;
                                                                                                                                                                                                                                                (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AVFKLLGFEPFSQRKLSTLKDESSR-----AWTESSIN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
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                                                                                                                                                                                            2000-329165/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVWVSSVFFFLPVFCLTVLYGLIGRKLWRRGRGDTAGGASLREQSHRQTVKMLAVVVFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLWVTTAYFFLFFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRQTKRVLLVVVLAF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AREGPGSAGWDLLP-----LFPAPLLAGVTATCVALFAVGVAGNLLTVLVVRRFREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFCWLPFHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLSAAINPILYNIMSKKYRV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECRPS--PAQLGALRV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TALSVERYFAICFPLRAKVLVTKGRVKLALLAIWAVAFCSAGPIFVLVGVEHE----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTTTNLYLCSLACSDLLIFLCMPLDLVRLWQYRPWTFGDLLCKLFQFVSEGCTYATVLTI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AREPP----WPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDM 69
                                                                                                                                                                                 AAA30643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-coupled receptor GHSR
                                                                                                                                                                                                                     Chalmers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                  99WO-US23938

 transmembrane domain 6; drug screening;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DPRD-----TRECRATEFAVRSGLLTA 195
                                                                                                                                                                                                                      GE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino

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RESULT 15
AAY70345
ID AAY70
XX
AC AAY70
XX
DT 20-JU
DT 20-JU
DX
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                                                                                                                                                                                                                                                                                       protein-coupled orphan receptor; GPCR; agonist;
PCR fusion protein; inverse agonist; drug; GHSR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS--PAQLGALRVMLWVTTAYFFLFFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHR 294
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                                                                                                                                                                                                                                                                                                                                                                                                   GHSR.
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human.
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30-OCT-1998;
04-DEC-1998;
26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses a method of identifying agonists and inverse or partial agonists to the endogenous, constitutively activated grotein-coupled orphan receptors (GPCRs), by contacting them with a GPCR fusion protein comprising a GPCR and a G protein. Determining expression of GPCRs in tissue samples can be used to identify related diseases. Inverse agonists to these receptors can be used as drugs for treating GPCR-related diseases. The present protein sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 123; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifying a compound against const
protein-coupled orphan receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human G protein-coupled orphan receptor, GHSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of a compound useful as a therapeutic agent, identifying a compound against constitutively activated G
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                                                                                                                                                                                                                                                                                           62 LLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRFWNFGDLLCKLFQF 121
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                                                                                                                                                                                                                                    VGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFL 176
PILYNIMSKKYRVAVFRLLGFEPFSQRKLSTLKDESSR--
                           PILYNLISKKYRAAAFKLLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN
                                                         QTVKMLAVVVFAFILCWLPFHVGRYLFSKSFEPGSLEIAQISQYCNLVSFVLFYLSAAIN
                                                                                                                   PTEFAVRSGLLTVMVMVSSIFFFLPVFCLTVLYSLIGRKLMRRRRGDAVVGASLRDQNHK 259
                                                                                                                                      PS--PAQUGALRVMLWVTTAYFFLPFICLSILYGLIGRELWSSRRPLRGPAASGRERGHR 294
                                                                                                                                                                                                      VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPSGPETAEAAALFSRECR 236
                                                                                    QTKRVLLVVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFYLSASIN
                                                                                                                                                                            VGVEHE----
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98US-0106300.
98US-0110906.
99US-0121851.
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Maximum DB seq length: 2000000000
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## ALIGNMENTS

FEATURES source		AUTHORS TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE	RESULT 1 EF513101 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
Location/Qualifiers 1590 /organism="Homo sapiens"	wmail: cgapbs-remail.nlh.gov Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: M13 Forward	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D.	human. human. Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 590)	BF513101 590 bp mRNA linear EST 07-DEC-2000 UI-H-BW1-amn-e-07-0-UI.sl NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070549 3', mRNA sequence. BF513101 BF513101.1 GI:11598280

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/clone=lib="NCI_CGAP_Sub7"
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/lab host="PROCE CF PROCE (Pharmacia) with a modified / note="Vector: pT73D-Pac (Pharmacia) with a modified / note="Vector: pT73D-Pac (Pharmacia) with a modified / note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI, NCI_CGAP_Sub6. The NCI_CGAP_Sub6 is a subtracted library had 12 million recombinants. A single-stranded DNA preparation of NCI_CGAP_Sub6 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI_CGAP_Kid5 pool 1 LLAM 333-342,372-3725, 3776-378 1322376-1323911, 1456008-1456775,1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-378 (IMAGE CloneIDS 123292-1325831, 1471368-147290), NCI_CGAP_Kid5 pool 1 LLAM 338-3342,3722-3725, 376-370, 1475104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3573-3582, 3851-3854 (IMAGE CloneIDS 1257096-1258631,1463064-1470983, 1475592-1476743); NCI_CGAP_PCD2 pool 1 LLAM 3573-3592, 3736-3720, 3733-3735 (IMAGE CloneIDS 1257096-1258631,1463064-1470983, 1475592-1476743); NCI_CGAP_PCD2 pool 1 LLAM 2457-2459, 1475592, 1476743); NCI_CGAP_PCD2 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 985608-98679, 2758-2759, 3062-3068 (IMAGE CloneIDS 985608-98679, 2758-2759, 3062-3068 (IMAGE CloneIDS 1057416-106125 LLAM 2457-2453), 2768-2759, 3062-3068 (IMAGE CloneIDS 705416-106125 LLAM 2457-2453), 2768-2759, 306616-2710535) and NCI_CGAP_Sub1 (IMAGE CloneIDS 271036-2713455) (10% of the driver population), plus a pool of 1,136 clones from NCI_CGAP_Sub1 (IMAGE CloneIDS 2712456) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE CloneIDS 2723969-2733190) (40% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE CloneIDS 2723969-2733190) (40% of the driver population), subtraction was performed as previously described (Bonaldo Lonende Soares (1995): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
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Box 166, Clay Center, NE 68933-0166, U
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                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pCMV SPORT6; Site 1: NotI; Site 2: Sall; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
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(db_xref="taxon:9913"

(clone_lib="MARC 3BOV"
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FEATURES
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AZ451922/c
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                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 504.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0251 row: C column: 06
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 bp DNA linear GSS 04-OCT-200100251C06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0251C06 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inserts
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                     clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0251C06"
                                                                                                                                                                                           lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                        sex="Male"
                                                                                                                                                                                                                                                                                                     strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                         organism="Mus musculus'
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SOURCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTCCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTTAAACTGCTGCTCGCAAGG 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI757121
603030882F1 NIH_MGC_114
                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                            Plate: LLAM11503 row: d column:
                                                                                                                                                                                                                                     http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 855)
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                                                                                                                                                                                      quality sequence stop: 803.
                                                                                                                                                                                                                                                         through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114)gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                  /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5200868"
                      /clone_lib="NIH_MGC_114"
/lab_host="DH10B"
                                                                                                                                                         Location/Qualifiers
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Pred. No. 6e-21;
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brain; Vector: pCMV-SPORT6;
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RESULT 5 BI757121

VERSION ACCESSION

KEYWORDS

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FEATURES

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium

REFERENCE

AUTHORS TITLE

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1010)

SOURCE

COMMENT

REFERENCE

AUTHORS

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BASE COUNT
ORIGIN
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                                                                         AGENCOURT 6625013 NIH MGC 114 Homo 5', mRNA sequence.
EM925480
 Homo sapiens
                                                        BM925480.1 GI:19375859
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Pred. No. 1.3e-17;
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Plate: LLAM12814 row: n column: 04
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/clone_lib="NIH_MGC_114"
/lab_bect_"ST165"
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GCTGAGCGTGGCAGGCCTGAGCGCCGAGCGCTGCCTAGCCGTGTGCCAGCCCCTGCGTGC
                                          CCTGCTCGGGCTGCCGTTCGACCTGTACCGCCTCTGGCGCTCGCGG----CCCTGGGTGTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCGTGGACACTCGCCTCTGGGCCAAGGTGCTGTTCACCGCGCTCTACGCACTCATCTG 168
                                                                                                                          CGGGCCGCTGCTCTGCCGCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCT
                                                                                                                                                                    GCTGGTCGGCGTGCGGGGGCTCTACAGCTTCGTGTGCTTCCACTACCCCTGGGTCTT
                                                                                                                                                                                                                                                    GCGAGCGGGCCTGCGCCACCACGTGCTCAGCCTGGCGCCTCGCGGGCCTGCTGCT
                                                                                                                                                                                                                                                                                                                                      GECGCTGEGCGCGGCCAATGCGCTGTCCGTGCACGTGGTGCTGAAGGCGCGGGCCGG
                                                                                                                                                                                                                                                                                                                                                                              CGTCGTCGGGGTGAGCGGCAACGTG-----GTGACCGTGATGCTGATCGGGGCGCTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTCGCCCTTTCCCCTGGGGGGGGCGCTGGTGCCGGTGACCGCTGTGTGCCTGTT 146
                                                                                  CGGCGACCTGGGCTGCCGGCTACTACTTCGTGCACGAGCTGTGCGCCTACGCCACGGT
                                                                                                                                                                                                                                                                                            GGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCAT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue_Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10671 row: g column: 03
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National Institutes of Health, M
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1 (bases 1 to 634)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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221 c 243 g 96 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:4792730"
/clone_lib="NIH MGC 96"
/tissue_type="hypothalamus"
/lab_host="DHIOB"
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GGACATGCGGACCACCACCACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCAT
                                                                                                                                                               GGGCGTGGACACTCGCCTCTGGGCCAAGGTGCTGTTCACCGCGCTCTACGCACTCATCTG 172
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AGENCOURT 6617918 NIH_MGC 124 Homo sapiens cDNA clone IMAGE:5734336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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National Institutes of Health,
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BM808829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1055)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library inormalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5734336"
/clone_lib="NIH_MGC_124"
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/lab_host="DH10B"
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Kim, N.S., Hahn, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 04
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Fax: +82-42-860-4409
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21C Frontier Korean
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           /note-Torgan: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt of the cDNA vector was selected manalized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
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/cell_line="SNU-5"
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                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Hisoscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov e column: 24
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1027)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT_6492823 NIH_MGC_124
                                                                                                                                                                                                                                                      Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726591"
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clone_lib="NIH_MGC_124"
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                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Tissue
                                                           Contact: Robert Strausberg, Ph.D
                                                                                                     Unpublished (1999)
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/lab_host="DH10B"
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CDNA Library Arrayed by: The I.M.A.G.E. Constrium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12726 row: e column: 02
Tetraodon
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/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Tetraodon nigroviridis.
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Bouneau,L., Billault,A.,
Weissenbach,J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C.,
Bernot, A., Fizames, C., Wincker, P., Brotties
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                         286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLAM12739 row: h column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT 6617870 NIH MGC 124 Homo 5', mRNA sequence
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence.
BM808823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence start: 84 quality sequence stop: 514.
Location/Qualifiers
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                             (note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library inormalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:5734333"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                  Score 119; DB 14;
Pred. No. 8.7e-16;
0; Mismatches 230
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REFERENCE
AUTHORS
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VERSION
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Best Local Similarity
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                      Department of Biological Sciences Graduate School of Science, Nagoya University Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan Tel: 81-52-789-2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanaka,E., Hori,H., Naruse,K., Mitani,H. and Tanaka,M. Medaka EST analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 bp mRNA linear EST 15-JAN-2002
AU244292 Medaka eye cDNA library (SNKO1) Oryzias latipes cDNA clone
NGY47.02e similar to pir|T15816|hypothetical protein C48C5.1 -
Caenorhabditis elegans, mRNA sequence.
                                                                                                                                                                                                                                                                                                                        Email: sanaka@bio.nagoya-u.ac.jp
This clone was isolated from Medaka
                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-52-789-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Emi Sanaka
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                                                                                  þ
                                                                                               Japan) "
                                                                                                                     /dev_stage="adult"
/note="Wild samples
                                                                                                                                                                                                   /organism="Oryzias latipes"
/strain="wild type"
/db_xref="taxon:8090"
/clone="NGY47.02e"
                                                                                                                                                             /clone_lib="Medaka eye cDNA library (SNK01)"
/tissue_type="eye"
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56.5%;
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1 (bases 1 to 738)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
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Contact: Robert Strausberg, Ph.D.
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/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcgag
                                                                                                          /clone="IMAGE:5288921"
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result beir and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a ter than or equal to the score of the result being printed,

SUMMARIES

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NO. 1 1 2 3 4 4 7 7 8 8	Score 119 119 103.6 102 102 102 102 102 103	Query Query Match Length 1212 5.8 1212 5.8 1212 5.0 1829 5.0 1829 5.0 1829 5.0 1829 5.0 2534	1 "	01 66 66 66 67 67	ID  US-10-083-168-13 US-10-083-168-82 US-09-104-063-5 US-09-905-186A-9 US-09-905-186A-11 US-10-087-345A-22 US-09-905-186A-1	Description  Sequence 13, Appl Sequence 82, Appl Sequence 5, Appli Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 22, Appl Sequence 11, Appl Sequence 11, Appl
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10	100.4	4.9	1829	9	US-09-905-186A-7	Sequence 7, Appli
11	100.4	4.9	1829	9	US-09-905-186A-8	Sequence 8, Appli
12	93.8	4.0	1258	10	US-09-804-551B-25	Sequence 25, App
14	93.6	4.4 5.6	1427	0 10	US-09-967-768A-296	Sequence 296, Ap
15	88.4	4.3	1647	10	US-09-829-631A-12	Sequence 12, App
16	88	4.3	1080	10	US-09-739-151-1	Sequence 1, Appl
17	88	4.3	1107	9	US-10-212-980-3	ω.
18	88	4.3	1185	10	US-09-993-844-13	Sequence 13, App
19	88	4.3	1417	9	US-10-007-132-3	Sequence 3, Appli

### ALIGNMENTS

RESULT 1 US-10-083-168-13

Sequence 13, Application US/10083168 Publication No. US20030023069A1 GENERAL INFORMATION:

Chen W.

Chalmers, Derek T.
Behan, Dominic P.
Maciejewski-Lenior, Dominique

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APPLICANT: Chalme
APPLICANT: Behan,
APPLICANT: Macie
APPLICANT: Leonat
APPLICANT: Ortune
APPLICANT: Lin,
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Best Local S
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CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively ACTITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1212
TYPE: DNA
ORGANISM: Homo sapiens
      270
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                                                                         CACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCCTGC---TCGG 269
GCCTACCAACTACCTCTTCAGCCTGGCCGTGTCGGACCTGCTGGTGCTGCTGGTGGG 269
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                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                       54.5%;
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RESULT 2 US-10-083-168-82

GENERAL INFORMATION:

Chen W.

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Liaw, APPLICANT: Chal

Ortuno, Daniel Lin, I-Lin Maciejewski-Lenior, Leonard, James N. Behan, Dominic P. Chalmers, Derek T.

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), OTHER INFORMATION: No. US20030023069Alel Sequence US-10-083-168-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/083,168
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 82
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 82, Application US/10083168 Publication No. US20030023069A1
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TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
TITLE OF INVENTION: Receptors
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0; Mismatches 215;
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Pred. No. 3.5e-20
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Length 1212;
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US-09-104-063-5
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                                                                                                                                    Matches 348;
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION UNMBER: 34,659
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, James
APPLICANT: Wood, WIlliam I.
TITLE OF INVENTION: PF4A Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/0 FILING DATE: 11-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415/25-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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    ACCGTGATGCTGATCGGGCGCTACCGGGACATGCGGACCACCACCAACTTGTACCTGGGC
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                                              GTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTCCTG
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48.7%;
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                                                                                                                                                        Score 103.6; DB 9
Pred. No. 3.1e-16;
                                                                                                                                                                               DB 9;
                                                                                                                                                                            Length 1679;
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Matches Query Match

261;

Conservative

54.5%;

Local Similarity

TYPE: DNA
ORGANISM: Unknown

LENGTH: 1212

FEATURE:

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US-09-823-114-18
; Sequence 18, Application US/09823114
; Patent No. US20020061554A1
; GENERAL INFORMATION:
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                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: CINKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 AAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTG
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APPLICATION NUMBER: 09/148,351
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: OPIOID RECEPTOR NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: EVANS, CHRISTOPHER J. KEITH, DUANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
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                                                                                                                                                              Sequence 9, Application US/09905186A Publication No. US20030008289A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
APPLICANT: Kreek, Mary Jeanne
APPLICANT: LaForge, Karl Steven
APPLICANT: LaForge, Karl Steven
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: FQ/No. US20030008289Aliceptin Receptor Gene, Diagnostic Methods
TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION UNVESER: US/09/905,186A
CURRENT FILING DATE: 2001-10-19
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Best Local Similarity
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SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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REGISTRATION NUMBER: 29,959
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LOCATION: 10..1119
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TELEX: 90-4030 MRSNFOERSWSH
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Pred. No. 8.3e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Appropriate Publication No.
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                                                                 Matches
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                          APPLICANT: LaForge, Karl Steven
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: FQ/No. US20030008289Ailceptin Receptor Gene, Diagnostic Method;
TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION NUMBER: US/09/905,186A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kreek, Mary Jeanne APPLICANT: LaForge, Karl Ste
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                                                                               Score 102; DB 9;
Pred. No. 8.3e-16;
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Best Local Similarity 51.0%;
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Pred. No. 8.3e-16;
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US-09-905-186A-10

TYPE: DNA
ORGANISM: homo

SOFTWARE: FastSEQ for Windows SEQ ID NO 10 LENGTH: 1829

Version

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SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
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Best Local
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TITLE OF INVENTION: ORPHANIN FQ RECEPTOR NUCLEIC
FILE REFERENCE: UM-06962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/087,345A
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2534
TYPE: DNA
ORGANISM: Homo sapiens
244 GTGTCCGACCTACTCCATCCTGCGGCCTCGCGCTTCGACCTGTACCGCCTCTGGCGCTCG
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                                                         GTCATCCTCAGGCACACAAAATGAAGACAGCCACCAATATTTACATCTTTAACCTGGCC 399
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US-09-905-186A-1
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LENGTH: 2602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kreek, Mary Jeanne
APPLICANT: LaForge, Karl Steven
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: FQ/No. US20030008289Aliceptin Receptor Gene, Diagnostic Methods
TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION NUMBER: US/09/905,186A
CURRENT APPLICATION NUMBER: US/09/905,186A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 11
NUMBER OF SEQ ID NOS: 11
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ORGANISM: homo sapiens
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ATGTTCACCAGCACCTTCACCCTAACTGCCATGAGTGTGGATCGCTATGTAGCCATCTGC
                                        ACCTACGCCACGCTGCACATGACCGCGCCTCAGCGTCGAGCGCTACCTGGCCATCTGC 423
                                                                                      GGCTTCTGGCCGTTTGGGAATGCGCTGTGCAAGACAGTCATTGCCATTGACTACTACAAC 1087
                                                                                                                                 CGGCCCTGGGTGTTCGGGCCGCTGCTCTGCCGCCTGTCCTCTACGTGGGCGAGGGCTGC 363
                                                                                                                                                                               CTGGCCGACACTCTGGTCCTGACGCTGCCCTT---CCAGGGCACGGACATCCTCCTG 1027
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RESULT 10 US-09-905-186A-7

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APPLICANT: Kreek, Mary Jeanne
APPLICANT: LaForge, Karl Steven
APPLICANT: LaForge, Karl Steven
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: PQ/No. US20030008289Allceptin Receptor Gene, Diagnostic Methods
TITLE OF INVENTION: Holes, and Methods of Treatment Based Thereon
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION NUMBER: US/09/905,186A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                              Sequence 25, Application US/09804551B Patent No. US20020056151A1
GENERAL INFORMATION:
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Sequence 7, Application US/09905186A Publication No. US20030008289A1 GENERAL INFORMATION:
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TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: FQ/No. US20030008289Aliceptin Receptor Gene, Diagnostic
TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION NUMBER: US/09/905,186A
CURRENT FILING DATE: 2001-10-19
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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LENGTH: 1829

Matches Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 296, Application US/09967768A Patent No. US20020150877A1 GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR APPLICATION NUMBER: US/60/236,111
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Best Local Similarity 51.1%;
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CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: DE 100 13 618.4
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 92
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NAME/KEY: CDS
LOCATION: (1)..(1257)
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TYPE: DNA
ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                     ; SEQ ID NO 3
; LENGTH: 1773
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10112599A
Publication No. US20030005476A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: DELTA OPIOID RECEPTOR DISRUPTIONS,
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING
FILE REFERENCE: R-678
                                                                                                              Query Match
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 296
LENGTH: 1427
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Best Local Similarity
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/280,513
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/112,599A CURRENT FILING DATE: 2002-09-05
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                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (135)...(1454)
NAME/KEY: misc_feature
LOCATION: (1)...(1647)
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US-09-829-631A-12
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LENGTH: 1647
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PRIOR APPLICATION NUMBER: US 08/428,242
PRIOR FILING DATE: 1995-09-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Parton
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TITLE OF INVENTION: The ST-B17 Serotonin Receptor
FILE REFERENCE: NIH047.1CP1C1
CURRENT APPLICATION NUMBER: US/09/829,631A
CURRENT FILING DATE: 2001-04-10
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                                                                                                                                                                                                                                                                 GGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGGCGCTACCGGGACATGCGGACCA 214
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                                                               CCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCCTGCTCGGGCTGC 274
                                                                                                                                                                         CGGCGGCGAACTCGCTGCTGATCGCGCTCATCTGCACTCAGCCCGCGCTGCGCAACA
                                                                                                                                                                                                                                                                                                                                                                  CCCGTCGNNNGGGGGGCAGCGGCTGGGTGGCGGCCTGTGCGTGGTCATCGCGCTGA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233;
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Pred. No. 2.1e-12;
0; Mismatches 244;
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Maximum Match 100%
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US-09-077-675A-14
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US-08-93-088A-4  Sequence 4, Application US/08993088A  Patent No. 6287855  GENERAL INFORMATION: APPLICANT: Tan, Carina APPLICANT: Sallivan, Kathleen TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND TITLE OF INVENTION: MUCLEGTIDES ENCODING SAME NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS; ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln Ave. CITY: Rahway STATE: NJ COUNTRY: USA ZIP: 07065-0900  COMPUTER: READABLE FORM: MEDIUM TYPE: Diskette COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER SYSTEM: Windows SOFTWARE: FASCESO for Windows SOFTWARE: FASCESO for Windows SOFTWARE: FASCESO for Windows SOFTWARE: FASCESO FOR WINDOWS APPLICATION NUMBER: US/08/93,088A FILING DATE: 18-DEC-1996 FILING DATE: 18-DEC-1996 FILING DATE: 27-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179 REFERENCE/DOCKET NUMBER: 38,179 REFERENCE/DOCKET NUMBER: 19846 TELEPHONE: 732-594-4720 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 283 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: Other FEATURE: NAME/KEY: Other FEATURE: NAME/FEATURE FEATURE MEDIUM/FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE F	28 106.6 5.2 1610 1 US-07-928-611-21 29 106.6 5.2 1610 2 US-08-487-811A-21 30 106.6 5.2 1610 4 US-09-060-694-21 31 106.6 5.2 1610 4 US-09-378-0774-21 32 106.6 5.2 1610 5 PCT-US93-07370-21 33 103.6 5.1 1679 1 US-08-076-093A-5 35 103.6 5.1 1679 1 US-08-701-265-5 36 103.6 5.1 1679 2 US-08-08-284-586-5 37 103.6 5.1 1679 2 US-08-805-478-5 39 103.6 5.1 1679 2 US-08-805-627A-5 40 103.6 5.1 1679 2 US-08-801-228-5 41 103.6 5.1 1679 2 US-08-801-228-5 42 103.6 5.1 1679 3 US-08-801-228-5 43 103.6 5.1 1679 3 US-08-801-228-5 44 103.6 5.1 1679 3 US-08-801-228-5 45 103.6 5.1 1679 3 US-08-801-228-5 46 103.6 5.1 1679 3 US-08-801-228-5 47 103.6 5.1 1679 3 US-08-801-228-5 48 103.6 5.1 1679 3 US-08-801-228-5 49 103.6 5.1 1679 3 US-08-801-228-5 40 103.6 5.1 1679 3 US-08-801-228-5 41 103.6 5.1 1679 3 US-08-801-228-5 42 103.6 5.1 1679 3 US-08-805-271A-18 45 102 5.0 1805 4 US-08-405-271A-18
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Patent No. 6337206
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERATE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,424B
FILLING DATE: 18-DEC-1997
CLASSIFICATION: 536
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APPLICANT: Kolakowski, Lee F., Jr.
TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
TYPE: nucleic acid
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NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,1
REFERENCE/DOCKET NUMBER:
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MEDIUM TYPE: Diskette
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                                                                     MOLECULE TYPE:
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TITY: Rahway
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                NAME/KEY:
LOCATION:
NAME/KEY: Other LOCATION: 1...283 OTHER INFORMATION:
                                                                                                                                                                                             TELEPHONE: 732-594-4720
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                                                                                                    STRANDEDNESS:
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P.O. Box 2000, 126 E. Lincoln Ave.
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                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                         NAME: COCUZZO, ARNA L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
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MEDIUM TYPE: Diskett
 MOLECULE TYPE:
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              YUENCE TO BE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOPOLOGY: linear
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ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merck & Co., Inc.
O. Box 2000, 126 E. Lincoln
                                                                                                                                                                                                                                                                                                                                        3-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 283;
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RESULT 4
US-09-077-675A-4
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                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pai, Le
APPLICANT: Feighne
APPLICANT: Howard
                                                                                                                                                                                                         ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 3-JUN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                         CITY:
STATE:
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln Ave
           NAME: Cocuzzo, Anna REGISTRATION NUMBER:
                                                         FILING DATE:
                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 CGCTCTTCCCCACGCCGCTGTTGGCGGGCGTCACCGCCACCTGCGTGGCGCCTCTTCGTGG 128
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T: Van Der Ploeg, Leonardus
INVENTION: RECEPTOR ASSAY
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Howard, Andrew D.
                                                                                                                                                                                       IBM Compatible
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Anna L. 42,452
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US-09-077-675A-9
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Pai, Le
APPLICANT: Heighnei
APPLICANT: Howard,
APPLICANT: Pong, SI
                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09077675A Patent No. 6242199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                  APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEPHAX: 732-594-4720
                                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                                                           STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
                                                                                                             ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Sim
hes 317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAACTCTTCCAGTTCGTTAGCGAGAGCTGCACCTACGCCACAGTGCTCACCATCACCG
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                                                                                                                                                                                                                                                                                                 Pai, Lee-Yuh
Feighner, Scott
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SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:

OPERATING SYSTEM:

APPLICATION NUMBER: FILING DATE: 3-JUN

3-JUN-1998

US/09/077,675A

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Patent No. (
                                                                                                                                                                                         Matches 316;
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1092 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080
                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                          92 CGCCCTTTCCCCTGGGGGCGCTGTGCCGGTGACCGCTGTGCCTGTTCCTCGTCG 151
                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 3-JUN-
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                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                           CGCTGTTCCCCGCTCCGCTGCTGGCAGGCGTCACCGCCACCTGCGTGGCGCTCTTCGTGG 163
 CCACCACCAACCTCTACCTGTCCAGCATGGCCTTCTCGGATCTGCTCATCTTCCTGTGCA 283
                                                            TGGGCATCTCAGGCAACCTGCTCACTATGCTGGTGGTGTCCCGCTTCCGGGAGCTGCGCA
                                                                                            TCGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGGCGCTACCGGGACATGCGGA 211
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                                                                                                                                                                                                          Similarity
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P.O. Box 2000, 126 E. Lincoln Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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Howard, Andrew D.
Pong, Sheng-Shung
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                        0;
                                                                                                                                                                                                          Score 228.4; DB 4; Pred. No. 7.3e-42;
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                                                                                                                                                                                           Mismatches 146;
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Вp
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
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REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 GCCCTTTCCCCTGGGGGGCGCTGGTGCCGGTGACCGCTGTGTGCCTGTGCCTGTTCGTCGT 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                   GTCCAGCATCTTCTTCCTTCCTGTCTTCTGTCTCACGGTCCTCTACAGTCTCATCGG 959
                                                                                                             CGCGGGCGCCACCGCCGTCCCCGCCGTCGGGGGCCCGAGACCGCGGAGGCCGCGGCGCTGT 691
                                                                                                                                                    CGAGTGCCGCCCCACCGAGTTTGCGGTGCGCTCTGGACTGCTCACGGTCATGGTGTGGGT 899
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                                                                                                                                                                                                                                                                TCCCTTCTTGTTCCTGGTGGGCGTCGAGCAGGACCCCGGCATCT-CCGTAGTCCCGGGCC 571
                                                                                                                                                                                                                                                                                                       CAAGGGGGGGGTGAAGCTGGTCATCTTCGTCATCTTGGGGCCGTGGCCCTTCTTGCAGCGCCGG
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; MOLECULE TYPE: US-09-077-675A-14
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US-09-077-675A-14
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                Query Match
Best Local Similarity
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Patent No. 6
    Matches
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APPLICANT: Pai, L.
                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                             NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07065-0900
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STREET: P.
                                                                                           TOPOLOGY:
                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                          ENGTH:
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    316;
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EDNESS: single
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                                                                                                                                     3129 base pairs
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Van Der Ploeg, Leonardus H.T.
NVENTION: RECEPTOR ASSAY
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                                                                                             linear
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
SYSTEM: DOS
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O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
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              11.2%;
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Score 228.4; DB 4;
Pred. No. 1e-41;
0; Mismatches 146;
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                              Length 3129;
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US-09-077-675A-6
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APPLICANT: Pal, Le
APPLICANT: Feighne:
APPLICANT: Howard,
APPLICANT: Pong, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09077675A Patent No. 6242199
                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
                               NAME: COCUZZO, ANDA L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                       FILING DATE: 3-JUN-19
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Van Der F
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: P.
                                                                                         NAME:
     TELEFAX:
                    TELEPHONE:
                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
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Howard, Andrew D.
Pong, Sheng-Shung
Van Der Ploeg, Leonardus
VENTION: RECEPTOR ASSAY
732-594-4720
                     732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                        Merck & Co., Inc.
O. Box 2000, 126 E.
                                                                                                                                                                                              3-JUN-1998
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INFORMATION FOR SEQ ID NO:

9

SEQUENCE CHARACTERISTICS:

LENGTH: 1080 L.
TYPE: nucleic acid
sing

1088 base pairs

; MOLECULE TYPE: cDNA
US-09-077-675A-6

STRANDEDNESS: sin TOPOLOGY: linear

single

Matches Query Match

93

Local Similarity nes 316; Conserv

Conservative

0

11.2%;

Score 227.8; DB Pred. No. 1e-41; Mismatches 147;

DB 4;

155

153

273 215

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CACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCCTGCTCGGGCT 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTTTCCCCTGGGGGCGCTGGTGCCGGTGACCGCTGTGCCTGTTCGTCGT 152
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US-09-545-944-1
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SOFTWARE: Fast
SEQ ID NO 1
LENGTH: 1248
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match (..., 68.9%; Best Local Similarity 68.9%; Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09545944
Patent No. 6461836
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: AMES, ROBERT
APPLICANT: ELSHOURBAGY, NABIL
APPLICANT: WICHALOVICH, DAVID
APPLICANT: SARAU, HENRY
APPLICANT: SHABON, USMAN
APPLICANT: SHABON, USMAN
APPLICANT: VANTER, LISA
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR
TITLE OF INVENTION: (AXOS34) AND SCREENING METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                   FILE REFERENCE: GP70657-1
CURRENT APPLICATION NUMBER: US/09/545,944
CURRENT FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 09/435,384
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
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Pred. No. 3.7e-25;
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US-09-077-675A-11

515 513 455

Sequence 11, Applicat Patent No. 6242199
GENERAL INFORMATION:

1, Application US/09077675A 6242199

COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: OF SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A

FILING DATE:

3-JUN-1998

ADDRESS:
ADDRESSE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.

STREET: P.O. CITY: Rahway

STATE:

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APPLICANT: Pai, Lee-Yuh
APPLICANT: Peighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Hong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

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US-08-858-876A-1
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Best Local Similarity 56.1%;
Matches 275; Conservative
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APPLICANT: I
APPLICANT: I
APPLICANT: V
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Type 2 Neurotensin Receptor
TITLE OF INVENTION: (hNT-R2)
NUMBER OF SEQUENCES: 12
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                                                                                                                                        CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                            APPLICATION NUMBER: US/08/858,876A
FILING DATE: 19-SEP-1997
                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                     Sequence 1, Application US/09472880 Patent No. 6274333 GENERAL INFORMATION: APPLICANT: Daniel CAPUT
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pair
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FILING DATE: 17-MAK-1...
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
NAME: Player, William E.
31,049
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STRANDEDNESS: single
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                           TITLE OF INVENTION: Type 2 Neurotensin (hNT-R2)
 CORRESPONDENCE
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SEQUENCES: 1:
DENCE ADDRESS
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Pred. No. 2.7e-19;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
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                                                                            CCGCAGCCTGACGCCACGCCGGACCCGGTGGCTGGTGGCGCTCTCGTGGGCCGCCTC
                                                                                                                                                CCGCGTCTTGGTCACCCGGGGCGCGCGTCGCGCGCGCTCATCGCTGTGCTCTGGGCCGTGGC 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jacobson, Price, Holman & Stern, STREET: 400 Seventh Street
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ZIP: 20004
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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Pred. No. 2.7e-19;
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RESULT 13
US-08-832-399-1
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APPLICANT: Bergsma, L
APPLICANT: Shabon, Us
TITLE OF INVENTION: N
NUMBER OF SEQUENCES:
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Patent No. 6008050
                                                                                                                                                                                                                                                                                                                              Query Match
-- Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GH50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUPTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/832.399
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                              GGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCAT
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 GCTGGTCGGCGTGGAACTCTACAGCTTCGTGTGGTTCCACTACCCCTGGGTCTT
                                                                GCGCGCGGGGCCCCGCCCACCACGTGCTCAGCCTGGCGCTCGCGGGCCTGCTGCTGCT
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55.0%;
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US-09-372-498-1
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APPLICANT: Derk J. Bergsma
APPLICANT: Usman Shabon
TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2
TITLE OF INVENTION: AND SPLICE VARIANTS THEROF
FILE REFERENCE: GH-50020-1
CURRENT APPLICATION NUMBER: US/09/372,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.1%;
Best Local Similarity 55.0%;
Matches 293; Conservative
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09372498 Patent No. 6166182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: 08/832,399
PRIOR FILING DATE: 1997-04-02
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ORGANISM: HOMO SAPIENS
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CCGCGTCTTGGTCACCCGGGCGCGCGCGCGCGCGCGCTCATCGCTGTGCTCTGGGCCGTGGC 497
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                                                                                               GCTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATCTGCCGCCCCGCTCCGCGC 437
                                                                                                                                     CCGCGACCTGGGCTGCCGCGGCTACTACTTCGTGCACGAGCTGTGCGCCTACGCCACGGT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125.4; DB 4; Length 1342; Pred. No. 5.8e-19; 0; Mismatches 231; Indels 9;
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                                                                                                                                                                                                                                                                                       Matches 292;
                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Player William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,876A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Type 2 Neurotensin Receptor TITLE OF INVENTION: (hNT-R2) NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Daniel CAPUT
APPLICANT: Pascale CHALON
APPLICANT: Pascual FERRARA
APPLICANT: Vita NATALIO
214 -ACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCCTGCTCG---
                                                       178 CACAGCGGGAATGCGCTGTCCGTGCACGTGGTGCTGAAGGCGGGGGCCGGTCGCCCCGG
                                                                                             156 GETGAGCGGCAACGTGGTGACCGTGATCCTGATCGGGGGCTACCGGGACATGCGGACC-- 213
                                                                                                                                        118
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                 36 GGGGGCGCGGAGCCGCCGTGGCCCGCCTGCCGCCTTGCGACGAGCGCCCGCTGCTCGCC
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                                                                                                                                                                        CTTTCCCCTGGGGGGCGCTGCCGGTGACCGCTGTGCCTGTTCCTTCGTCGTCGG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 GCTCTGCCGCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACAT 386
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538 TGCCCTGCCCATGGCGGTTATCATGGGACAGAAGCACGA 576
                                                                                                                          507 TGCCGGTCCCTTCTTGTTCCTGGTGGGCGTCGAGCAGGA 545
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Search completed: March 16, 2003, 10:51:09 Job time : 88 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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N Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Re

No.	Score	Query Match Length DB	Length		ID	Description
_	2040	100.0	2040	21	AAA46116	Human G protein co
N	2021.2	99.1	3066	22	AAZ45402	Genomic sequence o
w	1047.2	51.3	1161	22	AAF83684	Short form of moti
4	1047.2	51.3	1390	21	AAZ45404	cDNA encoding the
ហ	896.2	43.9	1239	21	AAZ45403	cDNA encoding the
σ	896.2	43.9	1239	22	AAF83683	Long form of motil
7	896.2	43.9	1239	22	AAF85449	Nucleotide sequenc
œ	896.2	43.9	1506	22	AA166989	Human GPR38 varian
9	669.8	32.8	1203	22	AAF85448	Nucleotide sequenc

## ALIGNMENTS

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RESULT 1
AAA46116
ID AAA4
  13-OCT-1998;
12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
16-FEB-1999;
26-FEB-1999;
12-MAR-1999;
12-MAR-1999;
                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                                                                                      Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                            13-OCT-1999;
                                                                                                                                                                               mutant; ss.
                                                                                                                                                                                                                   Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.
                                                                                                                                                                                                                                                         AAA46116;
                                                                                                                                                                                                                                                                           AAA46116 standard; cDNA; 2040
                                                                                                               20-APR-2000.
                                                                                                                                 WO200022131-A2
                                                                                                                                                                                                                                     22-AUG-2000 (first entry)
98US-0170496.
98US-0108029.
98US-0109213.
98US-0110060.
99US-01120416.
99US-0121852.
99US-0123944.
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Best Local Similarity
Matches 2040; Conserv
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12-MAR-1999
12-MAR-1999
12-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
30-JUN-1999
27-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic age
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29-SEP-1999;
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Liaw CW, Lin I, I
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100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the genomic sequence of the motilin creceptor gene, including the 5' untranslated region (5' UTR). This gene encodes a G-protein coupled receptor, and is designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A (see AAY54145) and MTL-R1B is a functional seven transmembrane domain form, and MTL-R1B is a truncated five transmembrane domain, The CMTL-R1B proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders, functional defects, infections, stress-related motility disorders, psychgenic disorders, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychgenic disorders, gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathis pseudo obstruction, acute faecal impaction, psyndrome, non-ulcer dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy, endoscopy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 2035;
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Pong S, Smith RG;
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CC receptor complex that involves providing an immobilized receptor, and CC contacting the receptor with a zsig33 peptide (comprising residues 24-37 CC of AB862649), where the receptor binds to the zsig33 peptide. The method CC is useful for purifying cells, purifying a peptide, stimulating signal CC transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, CC gastric contractility, nutrient uptake, secretion of digestive and CC pancreatic enzymes and hormones, secretion of digestive and CC I, secretion of non-zsig33 proteins. It is useful for modulating growth factor CC I, secretion in a mammal having a disease associated with abnormal CC remodeling, low osteoblast levels, cartilage repair and remodeling, CC skeletal dysplasia, immune suppression, obesity, growth retardation, CC dwarfism, wound healing and ovulation induction, treating a mammal having a mammal feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated CC gastrointestinal disorders, and stimulating glucose-induced insuling the protein secretion of meaning the name of secretion is still the protein catabolism and stimulating glucose-induced insuling the protein secretion of meaning the name of the protein secretion of meaning the name of the protein secretion of meaning the name of the protein secretion of meaning the name of the protein secretion of meaning the name of the protein secretion of meaning the name of the protein secretion of meaning the name of the protein secretion of meaning the name of the name of the protein secretion of the name of the protein secretion of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name of the name 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes splice variant MTL-R1B of the motilin receptor. The gene encodes a G-protein coupled receptor, and is designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1390 BP; 190 A; 496 C; 436 G; 268 T; 0 other;
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Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38; spliced form; MTL-R1B; gastric motility disorder; functional defect; neurological disorder; scleroderma; colonoscopy; paraneoplastic syndrome; radiation induced dysmotility; diabetes; infection; stress-related motility disorder; psychgenic disorder; gastroparesis; gastro-oesophageal reflux disease; constipation; chronic idiopathis pseudo obstruction; acute faecal impaction; postoperative ileus; gallstones; infantile collic; diarrhoea; postoperative lieus; gallstones; infantile collic; diarrhoea; irritable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable bowel syndrome; non-user dyspepsion; non-cardiac chest psintable syndrome; non-user dyspepsion; non-cardiac chest psintable syndrome; non-user dyspepsion; non-cardiac chest psintable syndrome; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non-user dyspepsion; non
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Matches 898
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                                                               Porming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                 zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-I; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R; ds;
                                          Disclosure; Page 102-104; 111pp; English
                                                                                                               WPI; 2001-355879/37.
P-PSDB; AAB62652.
                                                                                                                                                                                              22-NOV-1999;
                                                                                                                                                                                                                                                                    WO200138355-A2
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Long form of motilin receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF83683 standard; DNA; 1239
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The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, contacting the receptor with a zsig33 peptide (comprising residues

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Sequence 1239

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                                     The present sequence encodes a human motilin receptor polypeptide. The specification describes an unique sequence present in exon 1 of the dog motilin receptor, which is not present in human or Sphaeroides nephelus 7557 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect motilin receptor activity. Motilin receptor polymucleotides and polypeptides are used to identify therapeutic compounds which are useful for treating gastrointestinal diseases and disorders such as gastric motility disorders, gastroparesis, irritable bowel syndrome,
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gastroparesis; irr
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                                                                                                                                                                               Disclosure; Page 34; 42pp; English.
                                                                                                                                                                                                                    polypeptide, comprising unique regions from amino acid sequence, useful for identifying
                                                                                                                                                                                                                                                   Novel polypeptides related to dog and rabbit motilin receptor
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/note= "motilin receptor"
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compounds for treating
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Pred. No. 5.3e-174;
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Motilin receptor; gastrointestinal disease; gastric gastroparesis; irritable bowel syndrome; diarrhoea;
                                                                                                 Oryctolagus cuniculus
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WO200132710-A1.
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                                                                                                                                                                        sequence of a rabbit motilin receptor polypeptide
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                                          /*tag=
                                                                      Location/Qualifiers
                            note= "motilin receptor"
                                                                                                                                  motility disorder; ss.
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor amino acid sequence, useful for identifying compounds for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 18-19; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diarrhoea in humans
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       TGCACCTACGCCTGCCTGCCACATGACGGCGCTCAGCGTGGAGCGCTACCTGGCCATC
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Conservative
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Pred. No. 1.1e
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  The present sequence
                                                                                                 Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin remains acid sequence, useful for identifying compounds for trediarrhoea in humans
                                                 Claim 14; Page 17-18; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Motilin receptor; gastrointestinal disease; gastric motility disorder; gastroparesis; irritable bowel syndrome; diarrhoea; ss.
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Pred. No. 2.1e-101;
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XX Oligon
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                                                                                                                                                                                                                                                                                                            CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridisated to the two classes of oligomers, the degree of furthylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory CC systems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. CC ABQ11340-ABQ54121 represent genomic DNA sequences used to illustrate the CC method for determining the degree of cytosine methylation described in CC the disclosure of the invention.
                                                                                                                                 Matches 590;
                                                                                                                                                             Query Match
Best Local (
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                            Sequence 1179 BP; 178 A; 159 C; 443 G; 399
738
                                                                EPIGENOMICS
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                                                                                                                              Score 501.2; DB 24; Length 1179; Pred. No. 3.4e-93; 0; Mismatches 148; Indels 0;
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                                                                                                                                                                             Oligonucleotide for detecting cytosine methylation SEQ ID NO 33738.
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Query Match
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Similarity

21.4%; 74.5%;

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DB 24; Length

1179; 0;

Gaps

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Conservative

0;

Mismatches

Sequence 1179 BP; 462 A; 419 C; 159 G; 139 T; 0 other;

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3'; present in a genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of fiabels hybridised to the two classes of oligomers, the degree of fiabels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide contends of control and control of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

CC ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug; side effect; cancer; central nervous sy
gastrointestinal; respiratory system; single
SNP; cell differentiation; ds.
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
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                                 New human galanin receptor, GALR2, - useful to identify agonists antagonists to treat conditions involving galanin, e.g. for treatment of obesity or cognitive disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galanin receptor; GALR2; rat; ligand; obesity; anorexia; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galanin receptor GALR2 DNA probe.
                                                                                                                                                                                                        WPI; 1998-388039/33.
                                                                                                                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO INC.
(UYTE-) UNIV TEXAS HEALTH SCI
(UTOR ) UNIV TORONTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-1996;
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                                                                                                                                                                                                                                                                                    Kolakowski LF, O'Dowd B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 283 BP; 27 A; 116 C; 84 G; 56 T; 0 other;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

REFERENCE AUTHORS	ORGAINISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF034632	RESULT 1
<pre>1 (bases 1 to 2040) MCKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D., Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.</pre>	Homo Baptens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.	Homo sapiens.		AF034632.1 GI:2654158	AF034632	Homo sapiens orphan G protein-coupled receptor (GPR38) gene,	AF034632 2040 bp DNA linear PRI 13-JUL-1998		

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

TITLE

FEATURES

source

mRNA CDS

gene

TITLE JOURNAL

		1 GIGACCGCTGTGCCCTGTGCCTGTCGTCGTCGGGGTGAGCGGCAACGTGGTGACCGTG 180  1 ATGCTGATCGGGCGTACCGGGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATG 240  1	1 ATGGCAGCCCCTGGAACGGCAGCGACCCCCGAGGGGGCGCGGGAGCCCCCTGGCCGTGGCCC 60	Match 99.8*; Score 2035.2; DB 9; Length 2040; Jocal Similarity 99.9*; Pred. No. 1e-304; Score 2037; Conservative 0; Mismatches 3; Indels 0; Gaps 0; ATGGGCAGCCCCTGGAAGCGGAGCCCCCGAGGGGGGGGGG	YENI YALQLEYISASINE ILIYALI KAYRAAAFKILLARKSRPRGEHRSRDTAGEVAG DTGGDTVGYTETSANVKTMG" 347 a 631 c 598 g 464 t	CLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSNAVSDLLILLGLPFDLYRLWRSK PWVFGPLLCRLSLYVGEGCTYATILLMTALSVERYLALICRPLRARVLUVTRRRRVRALIA VLMAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSP PSGPETRARAALFSRECRPSPAQLGALRVLUVTTAYFFLPFLCLSILYGLIGRELMS GTEDL FOLDA & GTEDECHOTOTUBUT I NITHIA RETIVMI DE BEHUCET I TVI NITERSRAMVERGO GTEDL FOLDA & GTEDECHOTOTUBUT I NITHIA RETIVMI DE BEHUCET I TVI NITERSRAMVERGO	/product="GPR38" /protein_id="AAC26081.1" /db_xref="G1:2654159" /translation="MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAV	<pre>/gene="GPR38" /note="orphan G protein-coupled receptor related to growth hormone secretagogue and neurotensin receptors" /codon_start=1</pre>		/db_xref="taxon:9606" /chTomosome="13" /map="13g14-21" te <1>2040	Inc., PO Box 2000, Rahway, NJ 07065, USA Location/Qualifiers 1. 2040 /organism="Homo sapiens"	McKee, K.R Hreniuk, I Direct Su Submitted	E 2 (bases 1 to 2040)	Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA sequence from clone RP11-203116 on chromosome 13 Contains the gene for KIAA0970 protein, COX7CP1 (cytochrome c oxidase subunit VIIc pseudogene 1), a novel pseudogene, the GPR38 (G protein-coupled receptor 38) gene, ESTs, STSs, GSSs and a CpG island, complete sequence:
                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                        On Aug 29, 2000 this sequence version replaced gi:9926419. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; GPR38; KIAA0970.
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Eutheria; Primates;
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Further information can
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The true left end of clone RP11-103110 is at 1 in this sequence. This sequence has been finished according to sequence map sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203116 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VECTOR: pBACe3.6
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     /note="AluJo : 15007. .15361
                                                    14730.
                                                                                                                                                                                                                                                    13657. .13865
                                                                                                                                                                                                                                                                                                   13533. .13623
                                                                                                                                                                                                                                                                                                                                                  13303. .13348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2639.
6113. .6408
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="FLAM_C repeat: matches 2. .133 of consensus" 12875. .12887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 1. .301 of consensus" 4975. .5042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3240. .3621
/note="L2_repeat: matches 2310.
                                                                                                  /note="AluSg repeat: matches 1. .307 of consensus"
L4501. .14729
                                                                                                                                                                      /note="MLT1J repeat:
                                                                                                                                                                                                                     note="MLT1E repeat: matches 307.
                                                                                                                                                                                                                                                                    /note="MLT1E repeat: matches 223.
                                                                                                                                                                                                                                                                                                                                                                    /note="L1MB3 repeat: matches 5871. .6183 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 1530. .1542 of consensus"
12922. .13227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 1304. .1530 of consensus"
                                                                   'note="L1M4c repeat: matches 588. .813 of consensus"
                                                                                                                                                                                                                                                                                                                     note="MLT1E repeat: matches 1. .46 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12739. .1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="L2 repeat: matches 2704. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9887. .10191
/note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSc repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3824. .4106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1320. .1425
/note="MER94 repeat: matches 4. .114 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 137. .255 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 20. .137 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MER20 repeat: matches 4. .126 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluJo repeat: matches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-11.1"
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                                                 .15006
                                                                                                                                                    .14450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .12738
                                                                                                                                                                                                   14150
                       repeat:
                          matches 1.
                                                                                                                                                                         matches 195.
                    .285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .295 of consensus"
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                                                                                                                                                                         .456 of consensus
                                                                                                                                                                                                                          .533 of consensus"
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                                                                                                                                                                                                                                                                         consensus"
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note="HERVL repeat:

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> 27422. .27788 27029. .27259 26144. .26249

.28239

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29683. .29886 29448. .29681

3062

.30780

30324. .30620 29888.

.30323

misc\_feature

38014. .38191 36656. .36843

note="match: STS: Em:G04228" note="MIR repeat: matches 14.

. .38416

40037

.40103 .39708

40370

/note="L2 repeat: matches 2664. 10370. .40523

'note="MIR repeat: matches 34.

note="MER5A repeat: matches 7.

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/note="L2 repeat: matches 2626. 41549. .41871

/note="L2 repeat; matches 2242. 1085. .41156 /note="AluSx repeat: matches 2. note="L2 repeat: matches 2562.

/note="MER2 repeat: matches 1.

40811. .41080 40524. .40810 misc\_feature

36245

5. .36743 e="match: GSS: Em:AQ593229" e="AluSx repeat: matches 1.

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35454

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33134

1. .33214

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/note="L1M4c repeat: matches 813. .1178 of consensus" 15389. .15437 /note="L1M4c repeat: matches 1159. .1207 of consensus" 15438. .16412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30784. .30813
/note="15 copies 2 mer aa 86% conserved"
30814. .30947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mote="Lime3 repeat: matches 1. .310 of consensus"
28729. .29128
/note="Lime3 repeat: matches 4905. .5326 of conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26041. .26131
/note="FLAM_C repeat: matches 17. .107 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER5B repeat: matches 27. .79 of consensus"
17416. .17647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15800. .25825
/note="13 copies 2 mer tt 92% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2168. .2609 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 175. .262 of consensus"
35454. .35753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L2 repeat: matches 1879. .2259 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="L2 repeat: matches 2129. .2596 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L1ME3 repeat: matches 5724. .5874 of consensus"
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42192. .48502
/note="L1PA7 repeat: matches 128. .6143 of consensus"
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52190. .52379
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.0630. .50815
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CAGTACTTTAACATCGTCGCTCTGCAACTTTTCTATCTGAGCGCATCTATCAACCCAATC
                                                                                                                                                         TTCCACGTTGGCAGAATCATTTACATAAACACGGAAGATTCGCGGATGATGTACTTCTCT 1800
                                                                                                                                                                                                                                                            GGTGCTGTGTCTTATGTTGCAGTGGTGGTGGTTCTGGCATTTATAATTTGCTGGTTGCCC 146087
                                                                                                                                                                                                                                                                                                          GGTGCTGTGTCTTATGTTGCAGTGGTGGTGGTTCTGGCATTTATAATTTTGCTGGTTGCCC 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCTTGTTCAGAGAAATTGCTCCTTCTGGTTTATGTCCAGCCTTGATAACACATATGGG
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                                                                                                               TTCCACGTTGGCAGAATCATTTACATAAACACGGAAGATTCGCGGATGATGTACTTCTCT 146147
                                                                                                                                                                                                                                                                                                                                                                                                          GCAGATGGTTCCTTGTCGGGGGGGGGGGTTTATTTGCTTCCCAATGCTTTTGTTAATCCC 146027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGATGGTTCCTTGTCGGGGTGGGGGGGTTTATTTTGCTTCCCAATGCTTTTGTTAATCCC 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCTACTATGCAGTTTTAAAGCAAGTATCCATGCAGCCTGCAGCCTGGTCATTTTTTCT 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAGTAAACCTTGCTCGTATCAAAAAGTAAAGATTGTGCAGACCTGTTGTAGAATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGACGAGGGAGATTTCATTAAGCTAAAATTTTTTATTTAATGTTAAGTGATGCTGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACGAGGGAGATTTCATTAAGCTAAAAITTTTTTATTTAATGTTAAGTGATGCTGAAGGC 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCTACTATGCAGTTTTAAAGCAAGTATCCATGCAGCCTGCAGCCTGGTCATTTTTTCT 145907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCTTGTTCAGAGAAATTGCTCCTTCTGGTTTATGTCCAGCCTTGATAACACATATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTTAATCCAACCACCTGTTAGATGCCACAGATGAGGAGTCCTCACAGTGCTCTTGAGA
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FEATURES
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AUTHORS
TITLE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 149716 bases at least Q40 Consensus quality: 150039 bases at least Q30 Consensus quality: 150247 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 341360; sum-of-contigs
Insert size: 157238; 2.0% error; agarose-fp
Quality coverage: 3.92x in Q20 bases; sum-of-contigs Quality
coverage: 8.77x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: bA804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Aug 10, 2001 this sequence version replaced gi:15131387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 341560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number be preserved.
                                                                                                                                                                     146854 146953: gap of 100 bp
146954 338660: contig of 191707 bp in length
338661 338760: gap of 100 bp
338761 341560: contig of 2800 bp in length.
Location/Qualifiers
/clone="RP11-804"
/clone_lib="RPCI-11.1"
                                                                                        organism="Homo sapiens"/db_xref="taxon:9606"
                                                                chromosome="13"
                                                                                                                                                     .. .341560
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Qy 1981 ACTGGAGGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGATGGGATAA 2040	OY 1921 AAGTCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGGGAAGTTGCAGGGGAC 1980				QY 1681 GGTGCTGTGTCTTATGTTGCAGTGGTGGTGGTTCTGGCATTTATAATTTGCTGGTTGCCC 1740	QY 1621 GCAGATGGTTCCTTGTCGGGGTGGGGGGTTTATTTGCTTCCCAATGCTTTTGTTAATCCC 1680	QY 1561 GGGGTGAGGATCTGCCTAGGTAGAAGTTTTCTCTAATTTATTT	QY 1501 AGCCTACTATGCAGTTTTAAAGCAAGTATCCATGCAGCCTGGAGCCTGGTCATTTTTTCT 1560	OY 1441 CGGCTTGTTCAGAGAAATTGCTCCTTCTGGTTTATGTCCAGCCTTGATAACACATATGGG 1500	QY 1381 TTCAACAGAGAACAGAAAACTTGTCTCCGAAGTGGGTTTGTGGAAGGAA	OY 1321 TAAAGTAAACCTTGCTCGTATCAAAAAGTAAAGATTGTGCAGACCTGTTGTAGAATTCTT 1380	OY 1261 AGACGAGGGAGATTTCATTAAGCTAAAATTTTTTATTTAATGTTAAGTGATGCTGAAGGC 1320 	QY 1201 TTCTTAATCCAACCACCTGTTAGATGCCACAAATGAGGAGTCCTCACAGTGCTCTTGAGA 1260	QY 1141 CGATTCAGTAACCAGCAGTGCTTTTCCAGAGCCTCTGAGACCAGAAAGGAGAGTTGGTAA 1200 	OY 1081 TCCTGTCCCCCAGGAGCTCTGGGGGAACCCCCAGGGCGCTTTGAGGGTGGGATCCCCGGATC 1140	QY 1021 TTTCCTATTTCGATTCCAGCCTCCACCCGCCGGTACTTCCCCATCCCCCGAGAAAAACCATG 1080	QY 961 GCGCAAACGCTGGGTCCCCTTCCCCTGCTCGCCCAGCTCTGGGCGCCGCCTTCCAGCTCCC 1020	Qy 901 CGTAAGTGGAGCCGCCGTGGTTCCAAAGACGCCTGCCTGC

841 CTGCC	Qy 721 CAGCTGGGCGCGCTGCGTGTCATGCTGTGGTCACCACCGCCTACTTCCTTC	Qy 601 CCTCTCGCCTCGTCGCCGCCTCTTCGCCGGCGCGCCACCGCCGTCCCGCCGTCGCCGTCGCCGTCGCCGTCGCCGTCGCCGTCGCCGTCGCCGTCGCCGTCGCGTCGCGGCG	481 GTGCTCTGGGCGGTGGCGTGCTCTTGCCGGTCCTTGTTGT	Qy 361 TGCACCTACGCCACGCTGCTGCACATGACCGCGCTCAGCGTTCATCGGTT 480  Db 320144 TGCCGCCCGCGTCCCGCGCCCCGCGTCTTGGTTCACCCGGGCGCGCGC	QY 241 GCCGTGTCCGACCTACTCATCCTGCTCGGGCTGCCGTTCGACCTGTACCGCCTCTGGCGC 300	QY 121 GTGACCGCTGTGTGCCTGTGCCTGTTCGTCGTCGGGGGGACGGGCAACGTGGTGACCGTG 180		agment:03377.1"  agment:03476"  109064 t 200 others  2033.6; DB 2; Length 341560;  NO. 1.2e-304;  NO. 1.2e-304;  smatches 4; Indels 0; Gap
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TGCACCTACGCCACGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATC
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1 (Dases 1 to 1161)
Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D. Method of forming a peptide-receptor complex with zsig33 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZymoGenetics,
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AX154591
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/CLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLILLGLPFDLYRLWRSR
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VLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIASSPLALSSPPLWLSRAPPPSF
PSGPETABAALFSRECRPSPAQLGALRVMLWTTAYFFLPFLCLSILYGLIGRELWS
SRRPLRGPAASGRERGHRQTVRVLRKWSRRGSKDACLQSAPPGTAQTLGPLPLLAQLW
APLPAFFPISIPASTRRGGGSGIYNLLVALPRWQNHLHKHGRFADDVLLSVL"
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/db_xref="GI:14536178"
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Pred. No. 3.6e-35;
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1 (bases 1 to 1239)

Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D. Method of forming a peptide-receptor complex with zsig33 and Method of forming a peptide-receptor complex with zsig33 and
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PWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIA
                                                                                      /note="unnamed protein product"
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Submitted (16-MAY-1001) Microbiology
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Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Koti flanking sequences: a tool for gene discovery and verifical
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Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C., and Zabarovsky, E.R.
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Direct Submission
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1 (bases 1 to 615)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Kolthania, M., Wahlestedt, C. and Zabarovsky, E.R. Kisselev,L.L., Wasserman, W., Wahlestedt, G. and Zabarovsky, E.R. Motifianking sequences: a tool for gene discovery and verification
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Kutsenko, A. S., Gizatullin, R. Z., Al-Amin, A. N., Wang, F., Kvasha, S. M., Podowski, R. S., Gizatullin, R. Z., Gyanchandani, A., Muravenko, O. V., Levitsky, V. G., Kolchanov, N. A., Protopopov, A. I., Kashuba, V. I., Kisselev, L. L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E. R. NotI flanking sequences: a tool for gene discovery and verification of the human genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                          and Tumorbiology Centre,
3, Box 280, Stockholm 171
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AC109158.
AC109158.2 GI:20303716
AC109158.2 GI:20303716
HTG; HTGS PHASEZ; HTGS_DRAFT; HTG; HTG; HTGS_DRAFT; HTG; Mus musculus.
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Mus musculus clone RP24-199E5, V
                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 172168)
Birren, B., Linton, L., Nusbaum,
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/db xref="taxon:9606"
/clone="NR5-IP16C"
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Pred. No. 4.6e-56;
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                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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CE, 24 ordered
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TGCACCTACGCCACGCTGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACCCTGGCCATC

GCCGTGTCCGACCTACTCATCCTGCTCGGGCTGCCGTTCGACCTGTACCGCCTCTGGCGC GCCGTGTCCGACCTACTCATCCTGCTCGGGCTGCCGTTCGACCTGTACCGCCTCTGGCGC

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TGCNCGCCGCTCCGCGCGCGCGTTTGGGTCACCCGGCGCGCGCTNCGCGCGCGCTCATCGCT TGCCGCCCGCTCCGCGCCCCGCGTCTTGGTCACCCGGCGCCCCCGCTCCGCCGCCCCCATCGCT

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CAGGACCCCGGCATCTCCGTAGTCCCGGGCCTCAATGGCACCGCGCGGATCGCCTC

CANGACCCCCGCATTTCCGTAGTNCCCGGCCTTAATGGCACCGCGCGATATGCCTC

560

RESULT 9 HSA326768

SOURCE ORGANISM VERSION KEYWORDS

Homo sapiens

ACCESSION

DEFINITION

Homo sapiens ( NR5-IP16C. AJ326768

genomic

sequence

surrounding NotI site, DNA

701 bp

HSA326768

AJ326768.1

GI:15871186

REFERENCE

AUTHORS

PUBMED REFERENCE AUTHORS

Zabarovsky, E.R.

(bases 1 to 701)

Direct Submission
Direct Submission
Submitted (16-MAY-2001) Microbiology
Submitted (natitute, Theorells vag,

Sweden

Location/Qualifiers

JOURNAL

Nucleic Acids

Res. 30

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CE 3 (bases 1 to 172168)
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
RS Birren, B., Linton, L., Nusbaum, T., Boguslavkiy, L.,
Roward, R., Coke, P., DeArellano, K., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehozzky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Norbu, C., Netta, R., Rieback, M., Riley, R., Ise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Tavies, M., Tavisi, N., Tregilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zaihoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-APR-2002) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 25, 2002 this sequence version replaced gi:18482076. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center project name: L18656
Center clone name: 199 E 5
------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165710 bases at least Q40
Consensus quality: 165785 bases at least Q30
Consensus quality: 168675 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 172168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (25-APR-2002) Whitehead Institute/MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consists of 24 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence will be replaced
                                                                                                                                                                                                                                                                              107536 107635: gap of 100 bp
107636 131187: contig of 23552 bp
                                                                                                                                                                                                                                                                 131188 131287: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 8.4 in Q20 bases; agarose-fp Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                            152395 152494: gap of 100 b
152495 172168: contig of 19674
                                                                                                                                                                                                                                                                                                                                                                                         58023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 176000; agarose-fp
Insert size: 169868; sum-of-contigs
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31138 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8238
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1544. .2462
/note="assembly_fragment"
                                                            392. .1443
                                      /note="assembly_fragment'
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                          /db_xref="taxon:10090"
                                                                       note="assembly_fragment"
                                                                                                             'clone
                                                                                                                                                            organism="Mus musculus"
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8137: contig of 1066 bp in length
8237: gap of 100 bp
10569: contig of 2332 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23007:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      48247: ccm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0669: gap of 100 bp
13572: contig of 2903 i
3672: gap of 100 bp
16655: contig of 2983 i
6755: gap of 100 bp
                                                                                                                                                                                                                            1287: gap of 100 bp
152394: contig of 21107 b
2494: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                           147: gap of 100 bp
57922: contig of 9575 bp in length
322: gap of 100 bp
71628: contig of 13606 bp in length
                                                                                                                                                                                                                                                                                                                                                         90376:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp 31037: contig of 4674 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35: gap of 
22907: cont
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5453: contig of 1000 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1443: contig of 1052 bp in length
                                                                                                           _lib="RPCI-24 Male Mouse BAC"
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                                                                                                                                                                                                                                                                                                                                                                       gap of
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1: contig of 1418 bp in length
                                                                                                                                                                                                                                                                                                               p of 100 bp contig of 17059 bp in length
                                                                                                                                                                                                                                                                                                                                                   p of 100 bp contig of 18648 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 10083 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp
contig of 2172 bp in length
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/note="assembly\_fragment"
8238. .10569

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35613 Teerecceereaccaceererecccaaccrerrececeereeraraaeccaceree
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                                                                                                                                                                                                                                                                                                                          Score 307; DB 2; Length 172168;
Pred. No. 4.5e-38;
0; Mismatches 180; Indels 45;
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1 (bases 1 to 573)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M. Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muzavenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R. NotI flanking sequences: a tool for gene discovery and verificatio of the human genome
                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Zabarovsky, E.R.
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Nucleic acid encoding mouse galanin receptor
Patent: US 6337206-A 4 08-JAN-2002;
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Submitted (06-JUN-1996) Genetics & Molecular Biology, Merck
Research Laboratories, P.O. Box 2000, Building RY-80Y-265, J
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                     /translation="mmnatpseepgpnltlpdlgwdappendslveellplfptplla
GVTATCVALFVVGIAGNLLTMLVVSRFREMRTTTNLYLSSMAFSDLLIFLCMPLDLFR
LWQYRPWNLGNLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRV
                                                                                                                                                                                          /note="G-protein-alpha11 coupled receptor of pituitary hypothalamus; receptor for growth hormone releasing peptides (e.g.GHRP-6, GHRP-2) and non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
KLVILVIWAVAFCSAGPIFVLVGVEHDNGTDPRDTNECRATEFAVRSGLLTVMVWVSS
                                                                                             /product="growth hormone secretagogue receptor type la"
/protein_id="AAC48630.1"
/db_xref="GI:1504145"
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